

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:36:11 ; Search time 1125 Seconds

(without alignments)

10761.217 Million cell updates/sec

Title: US-10-813-588-1

Perfect score: 1464

Sequence: 1 atgacatctaagaattatcc.....caagtgatggcaggttaa 1464

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA Main:*
- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
 - 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
 - 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
 - 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
 - 6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
 - 7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
 - 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
 - 9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
 - 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB ID	Description
1	1464	100.0	9	US-10-813-588-1
2	1464	100.0	9	US-10-813-588-5
3	1464	100.0	9	US-10-813-588-3
4	1464	100.0	9	US-10-813-588-7
5	1462.4	99.9	1761	6 US-10-295-027-1083
6	1462.4	99.9	2010	6 US-10-295-027-1082
7	1462.4	99.9	2010	8 US-10-783-528-23
8	1462.4	99.9	2010	8 US-10-783-528-24
9	1459.8	99.7	2145	3 US-09-759-1308-72
10	1459.8	99.7	2145	7 US-10-741-790-72
11	1459.8	99.7	2888	7 US-10-312-352-47
12	1459.8	99.7	3151	5 US-10-003-132-1
13	1459.8	99.7	3594	3 US-09-759-1308-71
14	1459.8	99.7	3594	7 US-10-741-790-71
15	1459.8	99.7	3676	3 US-09-814-353-20367
16	1440.2	98.4	2547	6 US-10-108-260A-999
17	1107.4	75.6	2310	6 US-10-295-027-1084
18	1040.6	71.1	2145	5 US-10-003-132-12
19	584.2	39.9	2473	6 US-10-108-260A-2375
20	565.6	38.6	636	7 US-10-138-588-71
21	564.2	38.5	1538	7 US-10-138-588-69
22	548	37.4	596	8 US-10-696-639-1823
23	451.4	30.8	2836	5 US-10-003-132-3

24	449.8	30.7	1871	3	US-09-823-038A-43	Sequence 43, Appl
25	414.4	28.3	456	3	US-09-918-995-19131	Sequence 19131, A
26	400	27.3	400	8	US-10-696-639-1822	Sequence 1822, Ap
27	368.2	25.2	1509	5	US-10-003-132-13	Sequence 13, Appl
28	223	15.2	2868	5	US-10-003-132-5	Sequence 5, Appli
29	205.8	14.1	2310	6	US-10-191-436-4	Sequence 4, Appli
30	205.8	14.1	2310	6	US-10-191-436-6	Sequence 6, Appli
31	205.8	14.1	2310	10	US-11-055-679-4	Sequence 4, Appli
32	205.8	14.1	2310	10	US-11-055-679-6	Sequence 6, Appli
33	205.6	14.0	2020	6	US-10-094-749-861	Sequence 861, App
34	205.6	14.0	6595	8	US-10-723-860-6505	Sequence 6505, Ap
35	204	13.9	1962	5	US-10-060-830-1113	Sequence 1113, Ap
36	204	13.9	2190	5	US-10-060-830-2	Sequence 2, Appli
37	204	13.9	2200	7	US-10-451-010-13	Sequence 13, Appli
38	204	13.9	2280	5	US-10-060-830-1	Sequence 1, Appli
39	204	13.9	2328	6	US-10-191-436-1	Sequence 1, Appli
40	204	13.9	2328	6	US-10-191-436-3	Sequence 3, Appli
41	204	13.9	2328	10	US-11-055-679-1	Sequence 1, Appli
42	204	13.9	2328	10	US-11-055-679-3	Sequence 3, Appli
43	204	13.9	5657	3	US-09-974-298-96	Sequence 96, Appl
44	204	13.9	5657	5	US-10-084-817-65	Sequence 65, Appl
45	201.6	13.8	2428	5	US-10-106-698-1947	Sequence 1947, Ap

ALIGNMENTS

RESULT 1

US-10-813-588-1
; Sequence 1, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-1

Query Match 100.0%; Score 1464; DB 9; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT	60
Db	1	ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT	60
Qy	61	ACAGTACCAAGGGGAAAGACTGATTTCTGAGTTGGGAGATTTGGATATCGAATCCCAG	120
Db	61	ACAGTACCAAGGGGAAAGACTGATTTCTGAGTTGGGAGATTTGGATATCGAATCCCAG	120
Qy	121	ACCTGTGCTTCTGACTATCTTCTTACCAGCTCTTCAGATCAATATGGTCCATCTGT	180
Db	121	ACCTGTGCTTCTGACTATCTTCTTACCAGCTCTTCAGATCAATATGGTCCATCTGT	180

BEST AVAILABLE COPY

9, 10, 13, 14
for 9

QY 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTCGGGAATATGGTAGATGA 420
DB 517 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTCGGGAATATGGTAGATGA 576
QY 421 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATATTTCTGTATGAA 480
DB 577 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATATTTCTGTATGAA 636
QY 481 CTAGGTGGCCAGATCAGTGTCTTTCAGCGCAAGAGGATCAGTCGATATGAAGGATTTCTG 540
DB 637 CTAGGTGGCCAGATCAGTGTCTTTCAGCGCAAGAGGATCAGTCGATATGAAGGATTTCTG 696
QY 541 GCCAATGGTGTCTTTTCAGGAGATGGTTCTCTGACAGCAAGGATTTCTGTATGATCTC 600
DB 697 GCCAATGGTGTCTTTTCAGGAGATGGTTCTCTGACAGCAAGGATTTCTGTATGATCTC 756
QY 601 AATGGTTGCAAGATCCTTTGAGTTTGAACCTGACGGGCAATATCAGAGCTTTCTCTCA 660
DB 757 AATGGTTGCAAGATCCTTTGAGTTTGAACCTGACGGGCAATATCAGAGCTTTCTCTCA 816
QY 661 TGGCAGTTCGTCATCAGAGTGCAGACCAAGTTTCACTGGTCTCTGCGCAAGCCGACTT 720
DB 817 TGGCAGTTCGTCATCAGAGTGCAGACCAAGTTTCACTGGTCTCTGCGCAAGCCGACTT 876
QY 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACCAAGAG 780
DB 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACCAAGAG 936
QY 781 TGGCTGGAGATCGATTTGGGGAGAAAAAGAAATACAGGAATATAGGACCAAGATCT 840
DB 937 TGGCTGGAGATCGATTTGGGGAGAAAAAGAAATACAGGAATATAGGACCAAGATCT 996
QY 841 ACACAGTTCGAACCTTCAACTTTTATGTTTGAAGTTTGTGATGAATTTCAAAACATAT 900
DB 997 ACACAGTTCGAACCTTCAACTTTTATGTTTGAAGTTTGTGATGAATTTCAAAACATAT 1056
QY 901 TCTAAGTGAAGACCTTAAAGGAATGTGAATAATGAAGAAAGTGTTCAGGGTAAC 960
DB 1057 TCTAAGTGAAGACCTTAAAGGAATGTGAATAATGAAGAAAGTGTTCAGGGTAAC 1116
QY 961 TCTAAGTGAAGACCTTAAAGGAATGTGAATAATGAAGAAAGTGTTCAGGGTAAC 1020
DB 1117 TCTAAGTGAAGACCTTAAAGGAATGTGAATAATGAAGAAAGTGTTCAGGGTAAC 1176
QY 1021 CGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1080
DB 1177 CGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1236
QY 1081 CAGATTACAAAGGTAAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCAACAGTGT 1140
DB 1237 CAGATTACAAAGGTAAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCAACAGTGT 1296
QY 1141 TCACTTAAGAAAGAGATGAGACATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
DB 1297 TCACTTAAGAAAGAGATGAGACATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1356
QY 1201 GGAATAAACATTTACAGAGTGGCTATTTCCATTTGGTGTCTCTTGTGTTCTGTTTGTCT 1260
DB 1357 GGAATAAACATTTACAGAGTGGCTATTTCCATTTGGTGTCTCTTGTGTTCTGTTTGTCT 1416
QY 1261 GGAATGGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
DB 1417 GGAATGGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGTCCGTATGATCA 1476
QY 1321 GCGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCCAGACATCAG 1380
DB 1477 GCGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCCAGACATCAG 1536
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1440
DB 1537 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1596

QY 1441 ATCAACAAGTATATGCGAGTTAA 1464
DB 1597 ATCAACAAGTATATGCGAGTTAA 1620
RESULT 3
US-10-813-588-3
; Sequence 3, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-3
Query Match 100.0%; Score 1464; DB 9; Length 1761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCAGACTGTTTTCGAAAGACAAT 60
DB 298 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCAGACTGTTTTCGAAAGACAAT 357
QY 61 ACAGTACCAAAAGGGGAAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 120
DB 358 ACAGTACCAAAAGGGGAAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 417
QY 121 ACCTGTGCTTCTGACTATCTTCTTCAACAGCTCTTTCAGATCAATATGGTCCATCTGT 180
DB 418 ACCTGTGCTTCTGACTATCTTCTTCAACAGCTCTTTCAGATCAATATGGTCCATCTGT 477
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAGAGTGAAGTAAACCGTCCGCTTT 240
DB 478 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAGAGTGAAGTAAACCGTCCGCTTT 537
QY 241 GAGAGTGAATCCCAATTTCTGCGGGGTTTTCGTGACCTATTCGAGCAGCAGCAGCAT 300
DB 538 GAGAGTGAATCCCAATTTCTGCGGGGTTTTCGTGACCTATTCGAGCAGCAGCAGCAT 597
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 360
DB 598 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 657
QY 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTCGGGAATATGGTAGATGA 420
DB 658 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTCGGGAATATGGTAGATGA 717
QY 421 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATATTTCTGTATGAA 480
DB 718 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATATTTCTGTATGAA 777
QY 481 CTAGGTGGCCAGATCAGTGTCTTTCAGCGCAAGAGGATCAGTCGATATGAAGGATTTCTG 540

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Db 778 CTAGGTGGCCAGATCAGTGTGCTTCCAGCGCAAGGGATCAGTCGATATGAGGGATTCTG 837
Qy 541 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTCTCAGACAAGGATTTCTGTTCCTCC 600
Db 838 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTCTCAGACAAGGATTTCTGTTCCTCC 897
Qy 601 AATGGTTGACGAGATCTTGTAGTTTGAACCTTGACGGGCAATCAGAGCTTCTCTCA 660
Db 898 AATGGTTGACGAGATCTTGTAGTTTGAACCTTGACGGGCAATCAGAGCTTCTCTCA 957
Qy 661 TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTTCACTGTCTCTGCGCAAGCCGACTT 720
Db 958 TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTTCACTGTCTCTGCGCAAGCCGACTT 1017
Qy 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAAGGAG 780
Db 1018 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAAGGAG 1077
Qy 781 TGGCTGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 840
Db 1078 TGGCTGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1137
Qy 841 ACACAGTCGAATCTCAACTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 900
Db 1138 ACACAGTCGAATCTCAACTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 1197
Qy 901 TCTAAGTGAAGACCTATAAAGGAATTTGAATAAAGAAAAGGTGTTTCAGGGTAAC 960
Db 1198 TCTAAGTGAAGACCTATAAAGGAATTTGAATAAAGAAAAGGTGTTTCAGGGTAAC 1257
Qy 961 TCTAATCTTCGGGACCCAGTGCAACAAATTTCACTCCCTCCATCGTGGCCAGATATGT 1020
Db 1258 TCTAATCTTCGGGACCCAGTGCAACAAATTTCACTCCCTCCATCGTGGCCAGATATGT 1317
Qy 1021 CGGTTGTCTCCCGACAGATCGACAGAGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1318 CGGTTGTCTCCCGACAGATCGACAGAGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1377
Qy 1081 CAGATTACACAGGTAAATGATTTCAATTTGGTGTGGCGCAAGACAAGTCAAGACCAAGTGT 1140
Db 1378 CAGATTACACAGGTAAATGATTTCAATTTGGTGTGGCGCAAGACAAGTCAAGACCAAGTGT 1437
Qy 1141 TCAACTAAGAAAAGAGATGAGACATCAACAGGCCATCCCTCGGAAGAAAATCCACA 1200
Db 1438 TCAACTAAGAAAAGAGATGAGACATCAACAGGCCATCCCTCGGAAGAAAATCCACA 1497
Qy 1201 GGAATAAACATTACAACGGTGGCTATTTCCATTTGGTGTCTCTTGTGTCTGGTGTGCT 1260
Db 1498 GGAATAAACATTACAACGGTGGCTATTTCCATTTGGTGTCTCTTGTGTCTGGTGTGCT 1557
Qy 1261 GGAATGGGGATCTTTTGACGCTTTTGAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1558 GGAATGGGGATCTTTTGACGCTTTTGAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1617
Qy 1321 CGGAGGCTCAGAAAACAGACTGTGAGCAGATTAATATCCCTTTGCCAGACATCAG 1380
Db 1618 CGGAGGCTCAGAAAACAGACTGTGAGCAGATTAATATCCCTTTGCCAGACATCAG 1677
Qy 1381 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1678 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1737
Qy 1441 ATCACAAGTGATATGGCAGGTAA 1464
Db 1738 ATCACAAGTGATATGGCAGGTAA 1761
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RESULT 4

US-10-813-588-7

; Sequence 7, Application US/10813588

; Publication No. US20050053969A1

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

```
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-813-588-7
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Query Match 100.0%; Score 1464; DB 9; Length 1768;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAAAGACAAT 60
Db 59 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAAAGACAAT 118
Qy 61 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 120
Db 119 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 178
Qy 121 ACCTGTGCTTCTGACTATCTTCTCTTCCAGGCTCTTCAGATCAATATGGTCCCATCTGT 180
Db 179 ACCTGTGCTTCTGACTATCTTCTTTCACGAGCTCTTCAGATCAATATGGTCCCATCTGT 238
Qy 181 GGAAGTATGACTGTTCCTCAAAAGAACTCTTGTGTAACAACAGTGAAGTAAACCGTCCGCTTT 240
Db 239 GGAAGTATGACTGTTCCTCAAAAGAACTCTTGTGTAACAACAGTGAAGTAAACCGTCCGCTTT 298
Qy 241 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGACCTATGCGAGCAGGACCAT 300
Db 299 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGACCTATGCGAGCAGGACCAT 358
Qy 301 CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 360
Db 359 CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 418
Qy 361 TTCTGCCAGCTGGTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
Db 419 TTCTGCCAGCTGGTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 478
Qy 421 TATAGAGATACCTCTTTATTTGCAAAAGCTGCCATCCATGCAAGAAATAATTTGCTGTGATGA 480
Db 479 TATAGAGATACCTCTTTATTTGCAAAAGCTGCCATCCATGCAAGAAATAATTTGCTGTGATGA 538
Qy 481 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 540
Db 539 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 598
Qy 541 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTCAAGCAAGGATTTCTGTTCCTCC 600
Db 599 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTCAAGCAAGGATTTCTGTTCCTCC 658
Qy 601 AATGGTTGACGAGATCTCTTGTAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTCTCA 660
Db 659 AATGGTTGACGAGATCTCTTGTAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTCTCA 718
Qy 661 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTCTGCGCAAGCCGACTT 720
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Db	719	 TGGCAGTGGGTCAATGAGATGGGAGACCAAGTTCAC7GGTCTCTCGGCCAAGCCCGACTT	778
Qy	721	CAGGACCAAGGCCCATCATGGCTTCGGGGCGACAGTAGCAACAACCAACAACCCAGGAG	780
Db	779	CAGGACCAAGGCCCATCATGGCTTCGGGGCGACAGTAGCAACAACCAACAACCCAGGAG	838
Qy	781	TGGCTGGAGATCGAATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGGATCT	840
Db	839	TGGCTGGAGATCGAATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGGATCT	898
Qy	841	ACACAGTCGAACCTCAACTTTATGTTAAGAGTTTTCTGTGATGAACCTTCAAAAACAATAAT	900
Db	899	ACACAGTCGAACCTCAACTTTATGTTAAGAGTTTTCTGTGATGAACCTTCAAAAACAATAAT	958
Qy	901	TCTAAGTGGGAAGACCTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC	960
Db	959	TCTAAGTGGGAAGACCTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC	1018
Qy	961	TCTAACTTTTCGGGACCCAGTCGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGTG	1020
Db	1019	TCTAACTTTTCGGGACCCAGTCGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGTG	1078
Qy	1021	CGGGTTGTCCTCCCGACAGATCGCACAGAGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC	1080
Db	1079	CGGGTTGTCCTCCCGACAGATCGCACAGAGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC	1138
Qy	1081	CAGATTACACAGGTAAATGATTCATTGGTGTGGCGAAGACAAGTCAAAGCACCAAGTGT	1140
Db	1139	CAGATTACACAGGTAAATGATTCATTGGTGTGGCGAAGACAAGTCAAAGCACCAAGTGT	1198
Qy	1141	TCAACTAAGAAAGAATGAGACAATCACAAGGCCCATCCCTTCGGAAGAAACATCCACA	1200
Db	1199	TCAACTAAGAAAGAATGAGACAATCACAAGGCCCATCCCTTCGGAAGAAACATCCACA	1258
Qy	1201	GGAAATAACATTTACACGGTGGCTATTCCATTTGGTGTCTCTTGTGTCTGGTGTGTCT	1260
Db	1259	GGAAATAACATTTACACGGTGGCTATTCCATTTGGTGTCTCTTGTGTCTGGTGTGTCT	1318
Qy	1261	GGAAATGGGATCTTTGCAGCTTTAGAAAGAAGAAAGAAAGGAAGTCGGTATGATCA	1320
Db	1319	GGAAATGGGATCTTTGCAGCTTTAGAAAGAAGAAAGAAAGGAAGTCGGTATGATCA	1378
Qy	1321	CGCGAGGCTCAGAAAAACAGACTGTGGAAGCAGATTAAATATCCCTTTCGCCACATCAG	1380
Db	1379	CGCGAGGCTCAGAAAAACAGACTGTGGAAGCAGATTAAATATCCCTTTCGCCACATCAG	1438
Qy	1381	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAAGTTAGATCTC	1440
Db	1439	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAAGTTAGATCTC	1498
Qy	1441	ATCACAAAGTGATATGGCAGGTTAA	1464
Db	1499	ATCACAAAGTGATATGGCAGGTTAA	1522

RESULT 5

US-10-295-027-1083
; Sequence 1083, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

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Db      838  GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACACAGCGATTTCTGTGTACCTCC 997
Qy      601  AATGGTTGACGAGATCCTTGTAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 660
Db      898  AATGGTTGACGAGATCCTTGTAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 957
Qy      661  TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGGCCAAGCCGACTT 720
Db      958  TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGGCCAAGCCGACTT 1017
Qy      721  CAGGACCAAGGCCCATATGGGCTTCGGGGCAGTAGCAACAACAACAACACAGAG 780
Db      1018  CAGGACCAAGGCCCATATGGGCTTCGGGGCAGTAGCAACAACAACAACACAGAG 1077
Qy      781  TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 840
Db      1078  TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1137
Qy      841  ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 900
Db      1138  ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1197
Qy      901  TCTAAGTGGAGACCTATAAAGGAATTGCAATAATGAAGAAAAGTGTTCAGGGTAAC 960
Db      1198  TCTAAGTGGAGACCTATAAAGGAATTGCAATAATGAAGAAAAGTGTTCAGGGTAAC 1257
Qy      961  TCTAAGTGGAGACCTATAAAGGAATTGCAATAATGAAGAAAAGTGTTCAGGGTAAC 1020
Db      1258  TCTAAGTGGAGACCTATAAAGGAATTGCAATAATGAAGAAAAGTGTTCAGGGTAAC 1317
Qy      1021  CGGGTGTGTCCTCCAGACATGCGCACGAGATAGCTTGAAGGTGGAGCTCATTTGGTGC 1080
Db      1318  CGGGTGTGTCCTCCAGACATGCGCACGAGATAGCTTGAAGGTGGAGCTCATTTGGTGC 1377
Qy      1081  CAGATTACACAGGTAATGATTCATTGGTGTGGGCAAGACAAGTCAAGCACAGTGT 1140
Db      1378  CAGATTACACAGGTAATGATTCATTGGTGTGGGCAAGACAAGTCAAGCACAGTGT 1437
Qy      1141  TCAACTAAGAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAAACATCCACA 1200
Db      1438  TCAACTAAGAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAAACATCCACA 1497
Qy      1201  GGAATAAACAATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTGTCCTGGTGTGCT 1260
Db      1498  GGAATAAACAATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTGTCCTGGTGTGCT 1557
Qy      1261  GGAATGGGGATCTTTGACGCTTTAGAAAGAGAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db      1558  GGAATGGGGATCTTTGACGCTTTAGAAAGAGAGAAAGAAAGAAAGTCCGTATGGATCA 1617
Qy      1321  GCGAGGCTCAGAAAACAGACTGTTGAAGCAGATTAATATCCCTTTGCCAGACATCAG 1380
Db      1618  GCAGAGCTCAGAAAACAGACTGTTGAAGCAGATTAATATCCCTTTGCCAGACATCAG 1677
Qy      1381  TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGAGAGATGACACAAAAGTTAGATCTC 1440
Db      1678  TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGAGAGATGACACAAAAGTTAGATCTC 1737
Qy      1441  ATCAAGTGTATGGCAGGTAA 1464
Db      1738  ATCAAGTGTATGGCAGGTAA 1761
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RESULT 6

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US-10-295-027-1082
; Sequence 1082, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natesha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
```

```
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1082
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1082
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Query Match 99.9%; Score 1462.4; DB 6; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCAGACTGTTTGGGAAAAGACAATT 60
Db      282  ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCAGACTGTTTGGGAAAAGACAATT 341
Qy      61  ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 120
Db      342  ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 401
Qy      121  ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTTTCAGATCAATATGTCATCTGT 180
Db      402  ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTTTCAGATCAATATGTCATCTGT 461
Qy      181  GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAAGAGTAAGTAACCGTCGCTTT 240
Db      462  GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAAGAGTAAGTAACCGTCGCTTT 521
Qy      241  GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTGTCTGACCTATGCGAGCAGGACCAT 300
Db      522  GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTGTCTGACCTATGCGAGCAGGACCAT 581
Qy      301  CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 360
Db      582  CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 641
Qy      361  TTCTGCCAGCTGGTGTAGAGAGCTAGAGAGAGACATTTCTGGGAATATGGTAGATGA 420
Db      642  TTCTGCCAGCTGGTGTAGAGAGCTAGAGAGAGACATTTCTGGGAATATGGTAGATGA 701
Qy      421  TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTGCTGATGA 480
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Db 702 TATAGATACCTCTTTATTTGTCAGAAAGCTGCCATCCATGACGGAATAATTTGCTGATGAA 761
Qy 481 CTAGGTGGCCAGATCAGTGTCTTACGCGAAGAGGATCAGTGCATATGAAGGATCTG 540
Db 762 CTAGGTGGCCAGATCAGTGTCTTACGCGAAGAGGATCAGTGCATATGAAGGATCTG 821
Qy 541 GCCAATGGTGTCTTTTCGAGGATGTTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 600
Db 822 GCCAATGGTGTCTTTTCGAGGATGTTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 881
Qy 601 AATGGTTGACAGATCCTTGTAGTTTGAACCTGACGCGCAAAATCAGAGCTTCTTCTCA 660
Db 882 AATGGTTGACAGATCCTTGTAGTTTGAACCTGACGCGCAAAATCAGAGCTTCTTCTCA 941
Qy 661 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCACCTGCTCTGCGCAAGCCGACTT 720
Db 942 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCACCTGCTCTGCGCAAGCCGACTT 1001
Qy 721 CAGGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACCAAGAG 780
Db 1002 CAGGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACCAAGAG 1061
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGGATCT 840
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGGATCT 1121
Qy 841 ACACAGTCCGAACCTTCACTTTTATGTTTAAAGTTCCTGATGAACTTCAAAAACATAT 900
Db 1122 ACACAGTCCGAACCTTCACTTTTATGTTTAAAGTTCCTGATGAACTTCAAAAACATAT 1181
Qy 901 TCTAAGTGGAAAGCTTAAAGAAATTTGAATAATGAAGAAAGGTTTCAAGGTAAC 960
Db 1182 TCTAAGTGGAAAGCTTAAAGAAATTTGAATAATGAAGAAAGGTTTCAAGGTAAC 1241
Qy 961 TCTAAGTGGAAAGCTTAAAGAAATTTGAATAATGAAGAAAGGTTTCAAGGTAAC 1020
Db 1242 TCTAAGTGGAAAGCTTAAAGAAATTTGAATAATGAAGAAAGGTTTCAAGGTAAC 1301
Qy 1021 CGGGTTGTCCTCCAGACATGGCCAGAGGATAGCTTGAAGGTGAGCTCATTTGCTG 1080
Db 1302 CGGGTTGTCCTCCAGACATGGCCAGAGGATAGCTTGAAGGTGAGCTCATTTGCTG 1361
Qy 1081 CAGATTACCAAGGTAATGATTCATTTGTTGTCGCAAGCAAGTCAAGCAAGCTGTT 1140
Db 1362 CAGATTACCAAGGTAATGATTCATTTGTTGTCGCAAGCAAGTCAAGCAAGCTGTT 1421
Qy 1141 TCAACTTAAGAAAGATGAGCAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1422 TCAACTTAAGAAAGATGAGCAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1481
Qy 1201 GGAATAAACAATTACACGGTGGCTATTCATTTGTTGCTCTCTGCTGCTGTTGCT 1260
Db 1482 GGAATAAACAATTACACGGTGGCTATTCATTTGTTGCTCTCTGCTGCTGTTGCT 1541
Qy 1261 GGAATGGGATCTTTGAGGCTTTAGAAAGAAAGAAAGGATCCGATGATCA 1320
Db 1542 GGAATGGGATCTTTGAGGCTTTAGAAAGAAAGAAAGGATCCGATGATCA 1601
Qy 1321 GCGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCCAGACATCAG 1380
Db 1602 GCGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCCAGACATCAG 1661
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1440
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1721
Qy 1441 ATCAAGTGTATGTCAGGTTAA 1464
Db 1722 ATCAAGTGTATGTCAGGTTAA 1745

RESULT 7

US-10-783-528-23
; Sequence 23, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05892.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10783, 528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-783-528-23

Query Match 99.9%; Score 1462.4; DB 8; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGACATCTAAGAAATTTATCCCGGAGCTTACCCCAATCACACTGTTTCGCAAAAGACAATTT 60
Db 282 ATGACATCTAAGAAATTTATCCCGGAGCTTACCCCAATCACACTGTTTCGCAAAAGACAATTT 341
Qy 61 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 120
Db 342 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 401
Qy 121 ACCCTGCTCTTGACTATCTTCTTCCACAGCTCTTCCAGATCAATATGTTCCATCTGT 180
Db 402 ACCCTGCTCTTGACTATCTTCTTCCACAGCTCTTCCAGATCAATATGTTCCATCTGT 461
Qy 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTTCGAACAAGTGAAGTAAACCGTCCGCTTT 240
Db 462 GGAAGTATGACTGTTTCCCAAGAACTCTTGTTCGAACAAGTGAAGTAAACCGTCCGCTTT 521
Qy 241 GAGAGTGGATCCACATTTCTGCGCGGGGTTTTTCTGCTGACCTATGCGAGCAGGACCAT 300
Db 522 GAGAGTGGATCCACATTTCTGCGCGGGGTTTTTCTGCTGACCTATGCGAGCAGGACCAT 581
Qy 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGATAACAGCAA 360
Db 582 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGATAACAGCAA 641
Qy 361 TTCTGCGCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
Db 642 TTCTGCGCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 701
Qy 421 TATAGAGATACCTCTTTTATTTGCAAAAGCTGCCATCCATGCGAGGAATAATGCTGATGAA 480
Db 702 TATAGAGATACCTCTTTTATTTGCAAAAGCTGCCATCCATGCGAGGAATAATGCTGATGAA 761
Qy 481 CTAGGTGGCCAGATCAGTGTCTTACGCGAAGGATCAGTCGATATGAAGGATTTCTG 540
Db 762 CTAGGTGGCCAGATCAGTGTCTTACGCGAAGGATCAGTCGATATGAAGGATTTCTG 821
Qy 541 GCCAATGGTGTCTTTTCGAGGATGTTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 600
Db 822 GCCAATGGTGTCTTTTCGAGGATGTTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 881
Qy 601 AATGGTTGACAGATCCTTGTAGTTTGAACCTGACGCGCAAAATCAGAGCTTCTTCTCA 660
Db 882 AATGGTTGACAGATCCTTGTAGTTTGAACCTGACGCGCAAAATCAGAGCTTCTTCTCA 941
Qy 661 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCACCTGCTCTGCGCAAGCCGACTT 720
Db 942 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCACCTGCTCTGCGCAAGCCGACTT 1001
Qy 721 CAGGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACCAAGAG 780

Db 1002 CAGGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACACGAGAG 1061
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATTAACAGGAATTAGGACCAAGATCT 840
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATTAACAGGAATTAGGACCAAGATCT 1121
Qy 841 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTTCAAAAACAATAAT 900
Db 1122 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTTCAAAAACAATAAT 1181
Qy 901 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 960
Db 1182 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 1241
Qy 961 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 1020
Db 1242 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 1301
Qy 1021 CGGGTTGTCCCGAGACATGGCCACGAGGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1302 CGGGTTGTCCCGAGACATGGCCACGAGGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1361
Qy 1081 CAGATTACAAAGTAATGATTTCAATTTGGTGTGGGGAAGCAAGTCAAAGCACCATGTT 1140
Db 1362 CAGATTACAAAGTAATGATTTCAATTTGGTGTGGGGAAGCAAGTCAAAGCACCATGTT 1421
Qy 1141 TCAACTAAGAAAGAAAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1422 TCAACTAAGAAAGAAAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1481
Qy 1201 GGAATAAACATTACAAAGGTGGCTATTCCATTTGGTGTCTCTTGTGTTCTGGTGTGGCT 1260
Db 1482 GGAATAAACATTACAAAGGTGGCTATTCCATTTGGTGTCTCTTGTGTTCTGGTGTGGCT 1541
Qy 1261 GGAATGGGATCTTTGAGGCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1542 GGAATGGGATCTTTGAGGCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
Qy 1321 GCGAGGCTCAGAAACAGACTGTTGAAGCAGATTAATATCCCTTTGCGCAGACATCAG 1380
Db 1602 GCGAGGCTCAGAAACAGACTGTTGAAGCAGATTAATATCCCTTTGCGCAGACATCAG 1661
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAGAAAGAGATGACACAAAAGTTAGATCTC 1440
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATGAGAAAGAGATGACACAAAAGTTAGATCTC 1721
Qy 1441 ATCAAGTATATGGCAGGTTAA 1464
Db 1722 ATCAAGTATATGGCAGGTTAA 1745

RESULT 8
US-10-783-528-24
; Sequence 24, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783.528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent version 3.2
; SEQ ID NO 24
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-783-528-24

Query Match 99.9%; Score 1462.4; DB 8; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGAACAAAT 60
Db 282 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGAACAAAT 341
Qy 61 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 120
Db 342 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 401
Qy 121 ACCTGTGCTTCTGACTATCTTCTCTTACAGCTCTTTCAGATCAATATGGTCCATCTGT 180
Db 402 ACCTGTGCTTCTGACTATCTTCTCTTACAGCTCTTTCAGATCAATATGGTCCATCTGT 461
Qy 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCCGCTT 240
Db 462 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCCGCTT 521
Qy 241 GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTCTGACCTATGCGAGCAGCAGCAT 300
Db 522 GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTCTGACCTATGCGAGCAGCAGCAT 581
Qy 301 CAGATTAAATACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGAAATACAGCAA 360
Db 582 CAGATTAAATACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGAAATACAGCAA 641
Qy 361 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
Db 642 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 701
Qy 421 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATGACAGAAATATTTGCTGATGA 480
Db 702 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATGACAGAAATATTTGCTGATGA 761
Qy 481 CTAGGTGGCCAGATCAGTGTGCTTTCAGCCGAAAGGATCAGTCGATATGAAGGATCTG 540
Db 762 CTAGGTGGCCAGATCAGTGTGCTTTCAGCCGAAAGGATCAGTCGATATGAAGGATCTG 821
Qy 541 GCCAATGGTGTCTTTTCAGGGGATGTTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 600
Db 822 GCCAATGGTGTCTTTTCAGGGGATGTTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 881
Qy 601 AATGGTTGACAGATCTTTGATTTTGAACCTGTGAGGGCAATTCAGAGCTTCTTCTCTCA 660
Db 882 AATGGTTGACAGATCTTTGATTTTGAACCTGTGAGGGCAATTCAGAGCTTCTTCTCTCA 941
Qy 661 TGGCAGTCCGTCAATGAGGTGGAGCCCAAGTTTCACTGTTCTCTGCGCCAGCCGACTT 720
Db 942 TGGCAGTCCGTCAATGAGGTGGAGCCCAAGTTTCACTGTTCTCTGCGCCAGCCGACTT 1001
Qy 721 CAGGACCAAGCCCATCATCGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 780
Db 1002 CAGGACCAAGCCCATCATCGGCTTCGGGCGACAGTAGCAACCAACCAACGAGAG 1061
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATTAACAGGAATTAGGACCAAGATCT 840
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATTAACAGGAATTAGGACCAAGATCT 1121
Qy 841 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTTCAAAAACAATAAT 900
Db 1122 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTTCAAAAACAATAAT 1181
Qy 901 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 960
Db 1182 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 1241
Qy 961 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 1020
Db 1242 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAAGAAAGAGTTTTCAGGGTAAC 1301
Qy 1021 CGGGTTGTCCCGAGACATGGCCACGAGGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1080

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Db 1302 CGGGTGTGTCCTCCAGACATGGCCAGAGGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1361
Qy 1081 CAGATTACACAAGGTATGATTCATTTGGTGTGGGCAAGCAAGTCAAGCAGCAGTTT 1140
Db 1362 CAGATTACACNAGGTATGATTCATTTGGTGTGGGCAAGCAAGTCAAGCAGCAGTTT 1421
Qy 1141 TCAACTAAGAAAGAGATGAGACAATCACAAAGGCCATCCCTCGGAAGAAACATCCACA 1200
Db 1422 TCAACTAAGAAAGAGATGAGACAATCACAAAGGCCATCCCTCGGAAGAAACATCCACA 1481
Qy 1201 GGAATAAACATTAACAGGTGGGTATTCATTTGGTGTGGGCAAGCAAGTCAAGCAGCAGTTT 1260
Db 1482 GGAATAAACATTAACAGGTGGGTATTCATTTGGTGTGGGCAAGCAAGTCAAGCAGCAGTTT 1541
Qy 1261 GGAATCGGGATCTTTGAGAGCTTTTGAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1542 GGAATCGGGATCTTTGAGAGCTTTTGAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
Qy 1321 GCGAGGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1380
Db 1602 GCGAGGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1661
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGGAGATGACACAAAGTTAGATCTC 1440
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGGAGATGACACAAAGTTAGATCTC 1721
Qy 1441 ATCACAAGTGATATGCGAGCTTAA 1464
Db 1722 ATCACAAGTGATATGCGAGCTTAA 1745

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RESULT 9

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US-09-759-130B-72
; Sequence 72, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D.
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23

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; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-130B-72

Query Match 99.7%; Score 1459.8; DB 3; Length 2145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACACTCTTTGCGAAAAAGACAATT 60
Db 157 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACACTCTTTGCGAAAAAGACAATT 216
Qy 61 ACAGTACCAAAAGGGGAAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 120
Db 217 ACAGTACCAAAAGGGGAAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 276
Qy 121 ACCTGTCTCTGACTATCTTCTCTTCCAGAGCTCTTCCAGATCAATATGTCATCTGT 180
Db 277 ACCTGTCTCTGACTATCTTCTCTTCCAGAGCTCTTCCAGATCAATATGTCATCTGT 336
Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTTTGTTGAACACAGTCAAGTAAACCGTCCGCTTT 240
Db 337 GGAAGTATGACTGTTCCCAAGAACTCTTTGTTGAACACAGTCAAGTAAACCGTCCGCTTT 396
Qy 241 GAGAGTGGATCCCAATTTCTGCGGGGGTTTTTCTGCTACCTATGCGAGCAGCGACCAT 300
Db 397 GAGAGTGGATCCCAATTTCTGCGGGGGTTTTTCTGCTACCTATGCGAGCAGCGACCAT 456
Qy 301 CCAGATTATTAACATGTTTGGAAACAGAGCTAGCCATTTTGAAGACAGATACAGCAAA 360
Db 457 CCAGATTATTAACATGTTTGGAAACAGAGCTAGCCATTTTGAAGACAGATACAGCAAA 516
Qy 361 TTCTGCCAGCTGTTGTAGAGACGTAGCAGAGAGACATTTCTGGGAATATGGTAGATGA 420
Db 517 TTCTGCCAGCTGTTGTAGAGACGTAGCAGAGAGACATTTCTGGGAATATGGTAGATGA 576
Qy 421 TATAGAGATACCTCTTTATTTGTCAAAGCTGCCATCCATCCAGAGAAATAATTTGCTGATGA 480
Db 577 TATAGAGATACCTCTTTATTTGTCAAAGCTGCCATCCATCCAGAGAAATAATTTGCTGATGA 636
Qy 481 CTAGTGGCCAGATCAGTGTCTTCCAGCCAAAGGGATCAGTCGATATGAAGGGATCTG 540
Db 637 CTAGTGGCCAGATCAGTGTCTTCCAGCCAAAGGGATCAGTCGATATGAAGGGATCTG 696
Qy 541 GCCAATGGTGTCTTTCCAGGGGATGTTTCCCTGTGTCAGACAAGCATTTCTGTTTACCTCC 600
Db 697 GCCAATGGTGTCTTTCCAGGGGATGTTTCCCTGTGTCAGACAAGCATTTCTGTTTACCTCC 756
Qy 601 AATGGTTGCGAGAGATCTTTGAGTTTGAACCTGAGCGGCAAAATCAGAGCTTCTTCTCA 660
Db 757 AATGGTTGCGAGAGATCTTTGAGTTTGAACCTGAGCGGCAAAATCAGAGCTTCTTCTCA 816
Qy 661 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTTCACTGTCTCTGGCCAAAGCCGACTT 720
Db 817 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTTCACTGTCTCTGGCCAAAGCCGACTT 876
Qy 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGCAGTAGCAACAACCAACCAACCCAGAG 780
Db 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGCAGTAGCAACAACCAACCAACCCAGAG 936
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAAATAGGACCAAGGATCT 840
Db 937 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAAATAGGACCAAGGATCT 996
Qy 841 ACACAGTGGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTTCAAAAACAATAAT 900
Db 997 ACACAGTGGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTTCAAAAACAATAAT 1056

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QY 901 TCTAAGTGGAGACCTATAAAGGAATGTGAATAAGAAAAAGGTGTTTCAGGGTAAC 960
Db 1057 TCTAAGTGGAGACCTATAAAGGAATGTGAATAAGAAAAAGGTGTTTCAGGGTAAC 1116
QY 961 TCTAAGTGGAGACCTATAAAGGAATGTGAATAAGAAAAAGGTGTTTCAGGGTAAC 1020
Db 1117 TCTAAGTGGAGACCTATAAAGGAATGTGAATAAGAAAAAGGTGTTTCAGGGTAAC 1176
QY 1021 CGGGTGTGCTCCCGACATGCGCAGAGATAGCTTTGAAGGTGGAGCTCATTTGGTGTG 1080
Db 1177 CGGGTGTGCTCCCGACATGCGCAGAGATAGCTTTGAAGGTGGAGCTCATTTGGTGTG 1236
QY 1081 CAGATTACACAGGTAAATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCAACAGTGT 1140
Db 1237 CAGATTACACAGGTAAATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCAACAGTGT 1296
QY 1141 TCAACTAAGAAAGATGAGACATCAACAAGGCCCATCCCTCGGAGAAACATCCACA 1200
Db 1297 TCAACTAAGAAAGATGAGACATCAACAAGGCCCATCCCTCGGAGAAACATCCACA 1356
QY 1201 GGAATAACATTAACAAGGTGGCTTATTCATTTGGTGTGGCGCAAGACAAGTCAAAGCAACAGTGT 1260
Db 1357 GGAATAACATTAACAAGGTGGCTTATTCATTTGGTGTGGCGCAAGACAAGTCAAAGCAACAGTGT 1416
QY 1261 GGAATGGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGATGATCA 1320
Db 1417 GGAATGGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGATGATCA 1476
QY 1321 GCGAGGCTCAGAAACAGACTGTGGAAGCAGATTAATATCCCTTGGCAGACATCAG 1380
Db 1477 GCGAGGCTCAGAAACAGACTGTGGAAGCAGATTAATATCCCTTGGCAGACATCAG 1536
QY 1381 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1440
Db 1537 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1596
QY 1441 ATCAAGTGTATGGCAGTTA 1463
Db 1597 ATCAAGTGTATGGCAGTTA 1619

RESULT 10

US-10-741-790-72
; Sequence 72, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Gooden, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350MIM
; CURRENT APPLICATION NUMBER: US/10741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14

; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-790-72

Query Match 99.7%; Score 1459.8; DB 7; Length 2145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGACAAAT 60
Db 157 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGACAAAT 216
QY 61 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTTGGATATCGAATCCAG 120
Db 217 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTTGGATATCGAATCCAG 276
QY 121 ACCTGTGCTTCACTATCTTCTTTCACAGCTTTCAGATCAATATGTCATCTGT 180
Db 277 ACCTGTGCTTCACTATCTTCTTTCACAGCTTTCAGATCAATATGTCATCTGT 336
QY 181 GGAAGTATGACTGTTTCCCAAGAACTTTGTTGAAACACAGTGAAGTAAACCGTCCGCTTT 240
Db 337 GGAAGTATGACTGTTTCCCAAGAACTTTGTTGAAACACAGTGAAGTAAACCGTCCGCTTT 396
QY 241 GAGAGTGGATCCACATTTCTGCGCGGGTTTTGTGTAACCTATGCGAGCAGGACAT 300
Db 397 GAGAGTGGATCCACATTTCTGCGCGGGTTTTGTGTAACCTATGCGAGCAGGACAT 456
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGAAA 360
Db 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGAAA 516
QY 361 TTCTGCGCGAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
Db 517 TTCTGCGCGAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 576
QY 421 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCAGGAATAATTTGCTGATGAA 480
Db 577 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCAGGAATAATTTGCTGATGAA 636
QY 481 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTGCATATGAAGGATCTG 540
Db 637 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTGCATATGAAGGATCTG 696
QY 541 GCCAATGGTCTTTCTTTCAGGGATGTTCCCTGTTCAGACAGGATTTCTGTTTACCTCC 600
Db 697 GCCAATGGTCTTTCTTTCAGGGATGTTCCCTGTTCAGACAGGATTTCTGTTTACCTCC 756
QY 601 AATGTTTGCAGCAGATCTTTGAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCA 660
Db 757 AATGTTTGCAGCAGATCTTTGAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCA 816
QY 661 TGGCAGTGGGTCAATGAGAGTGGAGACAAAGTTCAGTGTCTCTGCGCAAGCCGACTT 720
Db 817 TGGCAGTGGGTCAATGAGAGTGGAGACAAAGTTCAGTGTCTCTGCGCAAGCCGACTT 876
QY 721 CAGGACCAAGGCCCATCATCTGCGGCTTCAGTGAAGCAACCAACCAACGAGAG 780

Db 877 CAGGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 936
Qy 781 TGCTGGAGATCGATTGGGGGAGAAAAGAAATACAGAAATAGGACCAAGATCT 840
Db 937 TGCTGGAGATCGATTGGGGGAGAAAAGAAATACAGAAATAGGACCAAGATCT 996
Qy 841 ACACAGTCGAACCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 997 ACACAGTCGAACCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1056
Qy 901 TCTAAGTGAAGACCTATAAGGAATTTGTAATTAAGAAAGAGTTTTCAGGGTAAC 960
Db 1057 TCTAAGTGAAGACCTATAAGGAATTTGTAATTAAGAAAGAGTTTTCAGGGTAAC 1116
Qy 961 TCTAAGTGAAGACCTATAAGGAATTTGTAATTAAGAAAGAGTTTTCAGGGTAAC 1020
Db 1117 TCTAAGTGAAGACCTATAAGGAATTTGTAATTAAGAAAGAGTTTTCAGGGTAAC 1176
Qy 1021 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1177 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1236
Qy 1081 CAGATTACACAGGTATGATTCATTTGGTGTGGCGAAGCAAGTCAAAGCACAGTGT 1140
Db 1237 CAGATTACACAGGTATGATTCATTTGGTGTGGCGAAGCAAGTCAAAGCACAGTGT 1296
Qy 1141 TCAACTAAGAAAGAGATGAGCAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1297 TCAACTAAGAAAGAGATGAGCAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1356
Qy 1201 GGAATAAACAATTACACGGTGGCTATTCATTTGGTGTCTCTCTGTTGCTGTTGCT 1260
Db 1357 GGAATAAACAATTACACGGTGGCTATTCATTTGGTGTCTCTCTGTTGCTGTTGCT 1416
Qy 1261 GGAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
Db 1417 GGAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1476
Qy 1321 GCGAGGCTCAGAAAACAGACTGTTGAAAGCAGATTAATATATCCCTTTCAGACATCAG 1380
Db 1477 GCGAGGCTCAGAAAACAGACTGTTGAAAGCAGATTAATATATCCCTTTCAGACATCAG 1536
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAAAGAGATGACACAAAAGTTAGATCTC 1440
Db 1537 TCAGCTGAGTTTACCATCAGCTATGATTAATGAAAGAGATGACACAAAAGTTAGATCTC 1596
Qy 1441 ATCACAAGTGATGGCAGTTA 1463
Db 1597 ATCACAAGTGATGGCAGTTA 1619

RESULT 11

US-10-312-352-47

; Sequence 47, Application US/10312352

; Publication No. US20040053824A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom

; APPLICANT: YUE, Henry; AZIMZAI, Yalda

; APPLICANT: HE, Ann; BATRA, Sajeev

; APPLICANT: LO, Terence P.; NGUYEN, Dammiel B.

; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.

; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.

; APPLICANT: LAL, Preeti G.; KEARNEY, Liam

; APPLICANT: BURFORD, Neil; YAO, Monique G.

; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.

; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.

; APPLICANT: BAUGHN, Mariah R.; HAPALIA, April, J.A.

; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.

; APPLICANT: LU, Yan; BOROWSKY, Mark L.

; APPLICANT: LU, Dyrung Aina M.; RAMKUMAR, Jayalaxmi

; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal

; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.

; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ekeane A.; THANGAVELU, Kavitha
; APPLICANT: DELEANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/21067
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,454
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/219,462
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 60/240,111
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/240,106
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/244,021
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/248,887
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/249,570
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 47
; LENGTH: 2888
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053824A1 184661CB1
US-10-312-352-47

Query Match 99.7%; Score 1459.8; DB 7; Length 2888;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTCCGAAAGACAAAT 60
Db 282 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTCCGAAAGACAAAT 341
Qy 61 ACAGTACCAAGGGGAAAAGACTGATTCAGAGTTGGGAGATTGGATATCGAATCCAG 120
Db 342 ACAGTACCAAGGGGAAAAGACTGATTCAGAGTTGGGAGATTGGATATCGAATCCAG 401
Qy 121 ACTGTGCTTTCAGATATCTTCTTTCACAGCTTTCAGATCAATATGGTCCATCTGT 180
Db 402 ACTGTGCTTTCAGATATCTTCTTTCACAGCTTTCAGATCAATATGGTCCATCTGT 461
Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT 240
Db 462 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT 521
Qy 241 GAGAGTGAATCCCAATTTCTGGCCGGGGTTTTTGTGCTGACCTATCCGAGCAGCGACCAT 300
Db 522 GAGAGTGAATCCCAATTTCTGGCCGGGGTTTTTGTGCTGACCTATCCGAGCAGCGACCAT 581
Qy 301 CCAGATTAAATACATGTTTGGAAAGAGCTAGCCATATTTGAAGAAGACAGAAACAGCAA 360
Db 582 CCAGATTAAATACATGTTTGGAAAGAGCTAGCCATATTTGAAGAAGACAGAAACAGCAA 641
Qy 361 TTCTGCCAGCTGTTGTAGAGACCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
Db 642 TTCTGCCAGCTGTTGTAGAGACCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 701
Qy 421 TATAGAGATACCTCTTTTATTTGCAAGCTGCGCATCCATCCAGCAAGTAAATTTGCTGATGA 480
Db 702 TATAGAGATACCTCTTTTATTTGCAAGCTGCGCATCCATCCAGCAAGTAAATTTGCTGATGA 761
Qy 481 CTAGTGGCCAGATCAGTGTGCTTTCAGCCAAAGGAGATCAGTCGATATGAAGGATCTTG 540
Db 762 CTAGTGGCCAGATCAGTGTGCTTTCAGCCAAAGGAGATCAGTCGATATGAAGGATCTTG 821

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QY 541 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTCACCTCC 600
Db      |||
QY 822 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTCACCTCC 881
Db      |||
QY 601 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCTCA 660
Db      |||
QY 882 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCTCA 941
Db      |||
QY 661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTCGCCCAAGCCGACATT 720
Db      |||
QY 942 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTCGCCCAAGCCGACATT 1001
Db      |||
QY 721 CAGGACCAAGGCCCATCATCGGGCTTCGGGCGACAGTAGCAACCAACCAACACGAGAG 780
Db      |||
QY 1002 CAGGACCAAGGCCCATCATCGGGCTTCGGGCGACAGTAGCAACCAACCAACACGAGAG 1061
Db      |||
QY 781 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATTAACAGGAATTAGGACCAAGGATCT 840
Db      |||
QY 1062 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATTAACAGGAATTAGGACCAAGGATCT 1121
Db      |||
QY 841 ACACAGTCGAACTCAACTTTTATGTTAAGAGTTTGTGATGAACCTCAAAAACAATAAT 900
Db      |||
QY 1122 ACACAGTCGAACTCAACTTTTATGTTAAGAGTTTGTGATGAACCTCAAAAACAATAAT 1181
Db      |||
QY 901 TCTAAGTGGAGACCTATAAAGCAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db      |||
QY 1182 TCTAAGTGGAGACCTATAAAGCAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1241
Db      |||
QY 961 TCTAAGTGGAGACCTATAAAGCAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1020
Db      |||
QY 1242 TCTAAGTGGAGACCTATAAAGCAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1301
Db      |||
QY 1021 CGGGTGTCTCCCGACATGGCACGACAGATAGCTTTGAGGTGGAGCTCATTTGGTTC 1080
Db      |||
QY 1302 CGGGTGTCTCCCGACATGGCACGACAGATAGCTTTGAGGTGGAGCTCATTTGGTTC 1361
Db      |||
QY 1081 CAGATTACACAGTAAATGATTCATTGGTGGGCGAAGCAAGTCAAAAGCACCAGTGT 1140
Db      |||
QY 1362 CAGATTACACAGTAAATGATTCATTGGTGGGCGAAGCAAGTCAAAAGCACCAGTGT 1421
Db      |||
QY 1141 TCAACTAAGAAAGAGATGAGACAAATCAAGGCCCATTCCTCGGAAGAAACATCCACA 1200
Db      |||
QY 1422 TCAACTAAGAAAGAGATGAGACAAATCAAGGCCCATTCCTCGGAAGAAACATCCACA 1481
Db      |||
QY 1201 GGAATAAACATTACAAAGGTGGCTATTCATTGGTGGTCTCTTGTGCTGGTGTGCT 1260
Db      |||
QY 1482 GGAATAAACATTACAAAGGTGGCTATTCATTGGTGGTCTCTTGTGCTGGTGTGCT 1541
Db      |||
QY 1261 GGAATGGGGATCTTTTCGAGCTTTAGAAAGAAAGAAAGAAAGGAAAGTCCGTATGGATCA 1320
Db      |||
QY 1542 GGAATGGGGATCTTTTCGAGCTTTAGAAAGAAAGAAAGAAAGGAAAGTCCGTATGGATCA 1601
Db      |||
QY 1321 GCGGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATAATCCCTTTGCCAGACATCAG 1380
Db      |||
QY 1602 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATAATCCCTTTGCCAGACATCAG 1661
Db      |||
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db      |||
QY 1662 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAAGTTAGATCTC 1721
Db      |||
QY 1441 ATCAAGATGATATGGCAGGTGA 1463
Db      |||
QY 1722 ATCAAGATGATATGGCAGGTGA 1744
Db      |||
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RESULT 12

US-10-003-132-1
; Sequence 1, Application US/10003132
; Publication No. US20020192750A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Gao, Zeren

; APPLICANT: Shoemaker, Kimberly E.
; TITLE OF INVENTION: NEUROFILIN HOMOLOG ZCUB5
; FILE REFERENCE: 00-62
; CURRENT APPLICATION NUMBER: US/10/003,132
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,004
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)...(2223)
US-10-003-132-1

Query Match 99.7%; Score 1459.8; DB 5; Length 3151;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGGAAAAGACAATT 60
Db      |||
QY 232 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGGAAAAGACAATT 291
Db      |||
QY 61 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 120
Db      |||
QY 292 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 351
Db      |||
QY 121 ACCTGTGCTTCACTATCTTCTCTTCAACAGCTCTTCAGATCAATATGTCATCTGT 180
Db      |||
QY 352 ACCTGTGCTTCACTATCTTCTCTTCAACAGCTCTTCAGATCAATATGTCATCTGT 411
Db      |||
QY 181 GGAAGTATGACTCTCCCAAGAACTCTTGTGTAACAACAAGTCAAGTAAACCGTCCGCTTT 240
Db      |||
QY 412 GGAAGTATGACTCTCCCAAGAACTCTTGTGTAACAACAAGTCAAGTAAACCGTCCGCTTT 471
Db      |||
QY 241 GAGAGTGGATCCCAACATTTCTGGCCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 300
Db      |||
QY 472 GAGAGTGGATCCCAACATTTCTGGCCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 531
Db      |||
QY 301 CGAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 360
Db      |||
QY 532 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 591
Db      |||
QY 361 TTCTGCCACCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
Db      |||
QY 592 TTCTGCCACCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 651
Db      |||
QY 421 TATAGAGATACCTCTTTTATTTGCAAAAGCTGCCATCCATCGAAGAAATATTTGCTGATGAA 480
Db      |||
QY 652 TATAGAGATACCTCTTTTATTTGCAAAAGCTGCCATCCATCGAAGAAATATTTGCTGATGAA 711
Db      |||
QY 481 CTAGGTGGCCAGATCACTGTCCTTCAGGCAAGGGATCAGTCGATATGAGGGATCTG 540
Db      |||
QY 712 CTAGGTGGCCAGATCACTGTCCTTCAGGCAAGGGATCAGTCGATATGAGGGATCTG 771
Db      |||
QY 541 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTCACCTCC 600
Db      |||
QY 772 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTCACCTCC 831
Db      |||
QY 601 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCA 660
Db      |||
QY 832 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCA 891
Db      |||
QY 661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACATT 720
Db      |||
QY 892 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACATT 951
Db      |||
QY 721 CAGGACCAAGGCCCATCATGCGGCTTCGGGCGACAGTAGCAACCAACCAACGAGAG 780
Db      |||
QY 952 CAGGACCAAGGCCCATCATGCGGCTTCGGGCGACAGTAGCAACCAACCAACGAGAG 1011
Db      |||
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QY 781 TGGCTGGAGATCGATTGGGGGAGAAAAAAGAAATACGGAATTAGGACACAGGATCT 840
Db 1012 TGGCTGGAGATCGATTGGGGGAGAAAAAAGAAATACGGAATTAGGACACAGGATCT 1071
QY 841 ACACAGTCGAACCTCAACTTTTATGTAAGAGTTTGTGATGAACATTCAAAAACAATAAT 900
Db 1072 ACACAGTCGAACCTCAACTTTTATGTAAGAGTTTGTGATGAACATTCAAAAACAATAAT 1131
QY 901 TCTAAGTGGAGACCTATAAGGAATGTCAATAATCAAGAAAGGTGTTTCAGGGTAC 960
Db 1132 TCTAAGTGGAGACCTATAAGGAATGTCAATAATCAAGAAAGGTGTTTCAGGGTAC 1191
QY 961 TCTAAGTGGAGACCTATAAGGAATGTCAATAATCAAGAAAGGTGTTTCAGGGTAC 1020
Db 1192 TCTAAGTGGAGACCTATAAGGAATGTCAATAATCAAGAAAGGTGTTTCAGGGTAC 1251
QY 1021 CGGGTGTCCCCAGACATGGCCACGAGATAGCCTTGAAGTGGAGCTCATTTGGTTGC 1080
Db 1252 CGGGTGTCCCCAGACATGGCCACGAGATAGCCTTGAAGTGGAGCTCATTTGGTTGC 1311
QY 1081 CAGATTACACAAGGTATGATTCATTGGTGTGGCGCAAGACAAAGTCAAGCACCAGTGT 1140
Db 1312 CAGATTACACAAGGTATGATTCATTGGTGTGGCGCAAGACAAAGTCAAGCACCAGTGT 1371
QY 1141 TCAACTAAGAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1372 TCAACTAAGAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1431
QY 1201 GGAATAAACAATTAACAAGGTGCTATTCATTCGGTGTCTCTGTTGTCCTGGTTGCT 1260
Db 1432 GGAATAAACAATTAACAAGGTGCTATTCATTCGGTGTCTCTGTTGTCCTGGTTGCT 1491
QY 1261 GGAATGGGATCTTTCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
Db 1492 GGAATGGGATCTTTCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1551
QY 1321 GCGAGGGCTCAGAAAAAGAGATGTTTGAAGCAGATTAATATATCCCTTTCAGACATCAG 1380
Db 1552 GCGAGGGCTCAGAAAAAGAGATGTTTGAAGCAGATTAATATATCCCTTTCAGACATCAG 1611
QY 1381 TCAGCTGAGTTTACCATCAGTATGATATAGAAAGAGATGACACAAAGTTAGATCTC 1440
Db 1612 TCAGCTGAGTTTACCATCAGTATGATATAGAAAGAGATGACACAAAGTTAGATCTC 1671
QY 1441 ATCACAAGTATGTCAGGTTA 1463
Db 1672 ATCACAAGTATGTCAGGTTA 1694

RESULT 13
US-09-759-1308-71
; Sequence 71, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiret, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-5350NIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16

; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 3594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-1308-71

Query Match 99.7%; Score 1459.8; DB 3; Length 3594;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACACTGTTTTCGAAAGACAAAT 60
Db 228 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACACTGTTTTCGAAAGACAAAT 287
QY 61 ACAGTACCAAGGGGAAAAAGACTGATTCGAGGTTGGGAGATTGGATATCGAATCCAG 120
Db 288 ACAGTACCAAGGGGAAAAAGACTGATTCGAGGTTGGGAGATTGGATATCGAATCCAG 347
QY 121 ACTGTGCTTTCGACTATCTTCTTCCACAGCTCTTCAGATCAATATGGTCCATCTGT 180
Db 348 ACTGTGCTTTCGACTATCTTCTTCCACAGCTCTTCAGATCAATATGGTCCATCTGT 407
QY 181 GGAAGTATCAGTGTTCCTCCAAAGAACTCTTGTGTAACACAGTGAAGTAAACCGTCCCTTT 240
Db 408 GGAAGTATCAGTGTTCCTCCAAAGAACTCTTGTGTAACACAGTGAAGTAAACCGTCCCTTT 467
QY 241 GAGAGTGAATCCCAATTTCTGGCCGGGGTGTTCCTGACCTATTCGAGCAGCAGCAT 300
Db 468 GAGAGTGAATCCCAATTTCTGGCCGGGGTGTTCCTGACCTATTCGAGCAGCAGCAT 527
QY 301 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATATTATTTGAAGACAGAAATACAGCAA 360
Db 528 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATATTATTTGAAGACAGAAATACAGCAA 587
QY 361 TTCTGCCAGCTGGTGTAGACAGCTAGCAGAGACATTTCTGGGAAATATGGTAGTGA 420
Db 588 TTCTGCCAGCTGGTGTAGACAGCTAGCAGAGACATTTCTGGGAAATATGGTAGTGA 647
QY 421 TATAGAGATACCTCTTTTATTTGCAAGCTGCATCCATCCATCGAGGAATAATTTGCTGATGA 480
Db 648 TATAGAGATACCTCTTTTATTTGCAAGCTGCATCCATCCATCGAGGAATAATTTGCTGATGA 707
QY 481 CTAGTGGCCAGATCAGTGTGCTTCAGCCAAAGGAGATCAGTCGATATGAAGGATTTCTG 540
Db 708 CTAGTGGCCAGATCAGTGTGCTTCAGCCAAAGGAGATCAGTCGATATGAAGGATTTCTG 767
QY 541 GCCAATGGTGTCTTTCGAGGGATGTTCCCTGTGACAGAAAGGATTTCTGTTTACCTCC 600
Db 768 GCCAATGGTGTCTTTCGAGGGATGTTCCCTGTGACAGAAAGGATTTCTGTTTACCTCC 827
QY 601 AATGGTTGACGAGATCCTTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCTCA 660

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Db      828  AATGGTTGACGAGATCCTTGGATTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 887
Qy      661  TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTCACTGGTCTCCTCGCCAAAGCCGACTT 720
Db      888  TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTCACTGGTCTCCTCGCCAAAGCCGACTT 947
Qy      721  CAGGACCAAGGCCCATCATCGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAG 780
Db      948  CAGGACCAAGGCCCATCATCGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAG 1007
Qy      781  TGCGTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 840
Db      1008  TGCGTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1067
Qy      841  ACACAGTCGAATCTCACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAAACAATA 900
Db      1068  ACACAGTCGAATCTCACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAAACAATA 1127
Qy      901  TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTA 960
Db      1128  TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTA 1187
Qy      961  TCTAAGTTCGGGACCCAGTGCAAAACAAATTTCAATCCCTCCATCGTGGCCAGATATG 1020
Db      1188  TCTAAGTTCGGGACCCAGTGCAAAACAAATTTCAATCCCTCCATCGTGGCCAGATATG 1247
Qy      1021  CGGGTGTCCCGACAGATCGCACCCAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTC 1080
Db      1248  CGGGTGTCCCGACAGATCGCACCCAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTC 1307
Qy      1081  CAGATTACACAGGTATGATTTCAATCGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1140
Db      1308  CAGATTACACAGGTATGATTTCAATCGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1367
Qy      1141  TCAACTAAGAAAGAGATGAGACAATCAACAGGCCCATTCCTCGGAAGAAAACATCCACA 1200
Db      1368  TCAACTAAGAAAGAGATGAGACAATCAACAGGCCCATTCCTCGGAAGAAAACATCCACA 1427
Qy      1201  GGAATRAACATTACAAGGTGGCTATTCCTATGGTGTCTCTTGTCTCTGGTGTGGT 1260
Db      1428  GGAATRAACATTACAAGGTGGCTATTCCTATGGTGTCTCTTGTCTCTGGTGTGGT 1487
Qy      1261  GGAATGGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db      1488  GGAATGGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1547
Qy      1321  GCGAGGCTCAGAAAACAGACTGTGGAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
Db      1548  GCGAGGCTCAGAAAACAGACTGTGGAGCAGATTAAATATCCCTTTGCCAGACATCAG 1607
Qy      1381  TCAGCTGAGTTTACCATCAGCTATGATAATCAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db      1608  TCAGCTGAGTTTACCATCAGCTATGATAATCAGAGGAGATGACACAAAAGTTAGATCTC 1667
Qy      1441  ATCAAAAGTATATGGCAGTTA 1463
Db      1668  ATCAAAAGTATATGGCAGATT 1690
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RESULT 14

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US-10-741-790-71
; Sequence 71, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kier, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
```

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; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 3594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-790-71
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Query Match 99.7%; Score 1459.8; DB 7; Length 3594;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTCGGAAGAACAAATT 60
Db      228  ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTCGGAAGAACAAATT 287
Qy      61  ACAGTACCAAGGGGAAAGACTGATTCAGAGTTGGGAGATTTGGGATATCGAATCCAG 120
Db      288  ACAGTACCAAGGGGAAAGACTGATTCAGAGTTGGGAGATTTGGGATATCGAATCCAG 347
Qy      121  ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGGTCCATCTGT 180
Db      348  ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGGTCCATCTGT 407
Qy      181  GGAAGTATGACTGTTCCTCAAGAACTCTTGTGAGCAAGAGTAAGTAACCGTCGCTTT 240
Db      408  GGAAGTATGACTGTTCCTCAAGAACTCTTGTGAGCAAGAGTAAGTAACCGTCGCTTT 467
Qy      241  GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTGTGCTGACTATGGAGCAGGACCAT 300
Db      468  GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTGTGCTGACTATGGAGCAGGACCAT 527
Qy      301  CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTTATTGGAAGACAGAAATACAGCAA 360
Db      528  CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTTATTGGAAGACAGAAATACAGCAA 587
Qy      361  TTCTGCCAGCTGGTCTGAGAGCTAGCAGGAGACATTTCTGGGAATATGTAGATCGA 420
Db      588  TTCTGCCAGCTGGTCTGAGAGCTAGCAGGAGACATTTCTGGGAATATGTAGATCGA 647
Qy      421  TATAGAGATACCTCTTTTATTGTGCAAAAGCTGCCATCCATGCCAGGAATTAATTTCTGATGAA 480
Db      648  TATAGAGATACCTCTTTTATTGTGCAAAAGCTGCCATCCATGCCAGGAATTAATTTCTGATGAA 707
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QY 481 CTAGTGGCCAGATCATGTGCTTACGCGAAAGGATCAGTCGATATGAAGGATCTG 540
Db |||||
QY 708 CTAGTGGCCAGATCATGTGCTTACGCGAAAGGATCAGTCGATATGAAGGATCTG 767
Db |||||
QY 541 GCGATGGTGTCTTTCGAGGATAGTTCCTGTGACAGGATTTCTGTTACTCTC 600
Db |||||
QY 768 GCGAATGGTGTCTTTCGAGGATAGTTCCTGTGACAGGATTTCTGTTACTCTC 827
Db |||||
QY 601 AATGGTTGACAGATCTTGAAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 660
Db |||||
QY 828 AATGGTTGACAGATCTTGAAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 887
Db |||||
QY 661 TGGCAGTCGTCATGAGAGTGAGACCAAGTTCTCTGTGCTCTGCGCCAAAGCCGACTT 720
Db |||||
QY 888 TGGCAGTCGTCATGAGAGTGAGACCAAGTTCTCTGTGCTCTGCGCCAAAGCCGACTT 947
Db |||||
QY 721 CAGGACAGGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 780
Db |||||
QY 948 CAGGACAGGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 1007
Db |||||
QY 781 TGGCTGGAGATCGATTGGGGGAGAAAAGAAATACAGGAATAGGACCAAGATCT 840
Db |||||
QY 1008 TGGCTGGAGATCGATTGGGGGAGAAAAGAAATACAGGAATAGGACCAAGATCT 1067
Db |||||
QY 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 900
Db |||||
QY 1068 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 1127
Db |||||
QY 901 TCTAAGTGGAGACCTATAAGGAATTGTGAATAAAGAAAGGTGTTTCAGGGTAAC 960
Db |||||
QY 1128 TCTAAGTGGAGACCTATAAGGAATTGTGAATAAAGAAAGGTGTTTCAGGGTAAC 1187
Db |||||
QY 961 TCTAAGTGGAGACCTATAAGGAATTGTGAATAAAGAAAGGTGTTTCAGGGTAAC 1020
Db |||||
QY 1188 TCTAAGTGGAGACCTATAAGGAATTGTGAATAAAGAAAGGTGTTTCAGGGTAAC 1247
Db |||||
QY 1021 CGGGTTGTCTCCCGACATGGCCACAGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db |||||
QY 1248 CGGGTTGTCTCCCGACATGGCCACAGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1307
Db |||||
QY 1081 CAGATTACACAAGGTATGATTCATTTGGTGTGGCGAAGAACAAAGTCAAAAGCACAGTTT 1140
Db |||||
QY 1308 CAGATTACACAAGGTATGATTCATTTGGTGTGGCGAAGAACAAAGTCAAAAGCACAGTTT 1367
Db |||||
QY 1141 TCAACTAAGAAAGAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db |||||
QY 1368 TCAACTAAGAAAGAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1427
Db |||||
QY 1201 GGAATAAACATTAACACGGTGGCTATTTCCATTGGTGTCTCTGTTGCTGCTGGTTGCT 1260
Db |||||
QY 1428 GGAATAAACATTAACACGGTGGCTATTTCCATTGGTGTCTCTGTTGCTGCTGGTTGCT 1487
Db |||||
QY 1261 GGAATGGGATCTTTGAGCTTTTGAAGAAAGAAAGAAAGTCCGTATGATCA 1320
Db |||||
QY 1488 GGAATGGGATCTTTGAGCTTTTGAAGAAAGAAAGAAAGTCCGTATGATCA 1547
Db |||||
QY 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTCGACACATCAG 1380
Db |||||
QY 1548 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTCGACACATCAG 1607
Db |||||
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGGAAGGAGATGACAAAAGTTAGATCTC 1440
Db |||||
QY 1608 TCAGCTGAGTTTACCATCAGCTATGATTAATGGAAGGAGATGACAAAAGTTAGATCTC 1463
Db |||||
QY 1441 ATCAAGTGTATGCGAGGTTA 1463
Db |||||
QY 1668 ATCAAGTGTATGCGAGGTTA 1690
Db |||||
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RESULT 15

US-09-814-353-20367

; Sequence 20367, Application US/09814353

; Publication No. US20030165831A1

; GENERAL INFORMATION:

; APPLICANT: Lee, John

; APPLICANT: Thompson, Pamela

; APPLICANT: Lillie, James

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

; FILE REFERENCE: MRI-006B

; CURRENT APPLICATION NUMBER: US/09/814,353

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/207,124

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: US 60/211,940

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: US 60/216,820

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/220,661

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/257,672

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 22037

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20367

; LENGTH: 3676

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 3676

; OTHER INFORMATION: n = A,T,C or G

; US-09-814-353-20367

Query Match 99.7%; Score 1459.8; DB 3; Length 3676;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTTCGAAAGACAAAT 60
Db 294 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTTCGAAAGACAAAT 353
QY 61 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGTTGGGAGATTTGATATCGAATCCCAG 120
Db 354 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGTTGGGAGATTTGATATCGAATCCCAG 413
QY 121 ACCTGTGCTTCTGACTATCTTCTTCCAGCTCTTCCAGATCAATATGTTCCATATCTGT 180
Db 414 ACCTGTGCTTCTGACTATCTTCTTCCAGCTCTTCCAGATCAATATGTTCCATATCTGT 473
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAAAGTGAAGTAAACCGTCCGCTTT 240
Db 474 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAAAGTGAAGTAAACCGTCCGCTTT 533
QY 241 GAGAGTGAATCCCAATTTCTGCGCGGGGTTTTTGTCTGACCTATTCGAGCAGCGACCAT 300
Db 534 GAGAGTGAATCCCAATTTCTGCGCGGGGTTTTTGTCTGACCTATTCGAGCAGCGACCAT 593
QY 301 CCAGATTTAATAACATGTTTGAAGCGAGCTAGCCATTTATTTGAAGAACAAGTAAACAGCAA 360
Db 594 CCAGATTTAATAACATGTTTGAAGCGAGCTAGCCATTTATTTGAAGAACAAGTAAACAGCAA 653
QY 361 TTCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGATATGTTAGTATGGA 420
Db 654 TTCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGATATGTTAGTATGGA 713
QY 421 TATAGATATACCTCTTTTATTTGTGCAAGCTGCCATCCATGCAGCAATATTTGCTGATGAA 480
Db 714 TATAGATATACCTCTTTTATTTGTGCAAGCTGCCATCCATGCAGCAATATTTGCTGATGAA 773
QY 481 CTAGTGGCCAGATCATGTGCTTACGCGAAAGGATCAGTCGATATGAAGGATCTG 540
Db |||||
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Db 774 CTAGGTGGCAGATCAAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCTG 833
Qy GCCAATGGTGTCTTTCGAGGGATGGTTCCTCTCAGACAAGCGATTTCCTGTTTACCTCC 600
Db 834 GCCAATGGTGTCTTTCGAGGGATGGTTCCTCTCAGACAAGCGATTTCCTGTTTACCTCC 893
Qy 601 AATGGTTGCAGCAGATCCCTTGAATTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCTCA 660
Db 894 AATGGTTGCAGCAGATCCCTTGAATTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCTCA 953
Qy 661 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCCAAGCCCGACTT 720
Db 954 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCCAAGCCCGACTT 1013
Qy 721 CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACAACCAACCAACCCAGAGAG 780
Db 1014 CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACAACCAACCAACCCAGAGAG 1073
Qy 781 TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGGAATTTAGGACCAAGATCT 840
Db 1074 TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGGAATTTAGGACCAAGATCT 1133
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 1134 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1193
Qy 901 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAAGGTGTTTTCAGGGTAAC 960
Db 1194 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAAGGTGTTTTCAGGGTAAC 1253
Qy 961 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAAGGTGTTTTCAGGGTAAC 1020
Db 1254 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAAGGTGTTTTCAGGGTAAC 1313
Qy 1021 CGGGTTGTCGCCAGACATGGCACCAGAGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1080
Db 1314 CGGGTTGTCGCCAGACATGGCACCAGAGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1373
Qy 1081 CAGATTACACAAGTAATGATTCAATTTGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGTT 1140
Db 1374 CAGATTACACAAGTAATGATTCAATTTGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGTT 1433
Qy 1141 TCAACTAAGAAAGAGATGAGACAATCAAGAAGGCCATCCCTCGGAAGAAAATCCACA 1200
Db 1434 TCAACTAAGAAAGAGATGAGACAATCAAGAAGGCCATCCCTCGGAAGAAAATCCACA 1493
Qy 1201 GGAATGGGGATCTTTGCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1260
Db 1494 GGAATGGGGATCTTTGCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1553
Qy 1261 GGAATGGGGATCTTTGCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1554 GGAATGGGGATCTTTGCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1613
Qy 1321 GCGAGGCTCAGAAAACAGACTGTTGGAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
Db 1614 GCGAGGCTCAGAAAACAGACTGTTGGAGCAGATTAAATATCCCTTTGCCAGACATCAG 1673
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1674 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1733
Qy 1441 ATCAAGTGAATATGGCAGTTA 1463
Db 1734 ATCAAGTGAATATGGCAGTTA 1756

Search completed: January 15, 2006, 19:46:31
Job time : 1129 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:53:27 ; Search time 949 Seconds
(without alignments)

4243.611 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNYPGTYPNHTVCEKTI.....YDNEKEMTKQLDLITSDMAG 487

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134683005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlp

-Q=/cgn2_1/USPTO_spool_p/US10813588/runat_12012006_171132_15445/app_query.fasta_1.647

-DB=Published Applications NA_Main -QFMT=fastap -SUFFFIX=p2n.rnpbm

-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1

-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct

-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext

-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

-USER=US10813588 @CGN_1_1_1549 @runat_12012006_171132_15445 -NCPU=6 -ICPU=3

-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA_Main:

1: /cgn2_6/ptodata1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata1/pubpna/US09B_PUBCOMB.seq:*
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9: /cgn2_6/ptodata1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2557	100.0	1464	9	US-10-813-588-1
2	2557	100.0	1620	9	US-10-813-588-5
3	2557	100.0	1761	6	US-10-295-027-1083
4	2557	100.0	1761	9	US-10-813-588-3
5	2557	100.0	1768	9	US-10-813-588-7
6	2557	100.0	2010	6	US-10-295-027-1082
7	2557	100.0	2010	8	US-10-783-528-23

8	2557	100.0	2010	8	US-10-783-528-24	Sequence 24, Appl
9	2551	99.8	2145	3	US-09-759-1308-72	Sequence 72, Appl
10	2551	99.8	2145	7	US-10-741-790-72	Sequence 72, Appl
11	2551	99.8	2888	7	US-10-312-352-47	Sequence 47, Appl
12	2551	99.8	3151	5	US-10-003-132-1	Sequence 1, Appl
13	2551	99.8	3594	3	US-09-759-1308-71	Sequence 71, Appl
14	2551	99.8	3594	7	US-10-741-790-71	Sequence 71, Appl
15	2551	99.8	3676	3	US-09-814-153-20367	Sequence 20367, A
16	2512.5	98.3	2547	6	US-10-108-260A-999	Sequence 999, App
17	2259	88.3	2310	6	US-10-108-260A-1084	Sequence 1084, Ap
18	2020	79.0	2145	5	US-10-003-132-12	Sequence 12, Appl
19	1313.5	51.4	1538	7	US-10-138-588-69	Sequence 69, Appl
20	1154.5	45.2	2836	5	US-10-003-132-3	Sequence 3, Appl
21	1146.5	44.8	1871	3	US-09-823-038A-43	Sequence 43, Appl
22	1003	39.2	2473	6	US-10-108-260A-2375	Sequence 2375, Ap
23	989	38.7	636	7	US-10-138-588-71	Sequence 71, Appl
24	974	38.1	596	8	US-10-696-639-1823	Sequence 1823, Ap
25	920	36.0	2868	5	US-10-003-132-5	Sequence 5, Appl
26	881.5	34.5	1509	5	US-10-003-132-13	Sequence 13, Appl
27	867.5	33.9	2310	6	US-10-191-436-7	Sequence 7, Appl
28	867.5	33.9	2310	6	US-10-191-436-9	Sequence 9, Appl
29	867.5	33.9	2310	10	US-11-055-679-7	Sequence 7, Appl
30	867.5	33.9	2310	10	US-11-055-679-9	Sequence 9, Appl
31	860.5	33.7	2190	5	US-10-060-830-2	Sequence 2, Appl
32	860.5	33.7	2280	5	US-10-060-830-1	Sequence 1, Appl
33	860.5	33.7	2328	6	US-10-191-436-1	Sequence 1, Appl
34	860.5	33.7	2328	6	US-10-191-436-3	Sequence 3, Appl
35	860.5	33.7	2328	10	US-11-055-679-1	Sequence 1, Appl
36	860.5	33.7	2328	10	US-11-055-679-3	Sequence 3, Appl
37	860.5	33.7	5657	3	US-09-974-298-96	Sequence 96, Appl
38	860.5	33.7	5657	5	US-10-084-817-65	Sequence 65, Appl
39	860.5	33.7	6595	8	US-10-723-860-6505	Sequence 6505, Ap
40	856.5	33.5	2310	6	US-10-191-436-4	Sequence 4, Appl
41	856.5	33.5	2310	6	US-10-191-436-6	Sequence 6, Appl
42	856.5	33.5	2310	10	US-11-055-679-4	Sequence 4, Appl
43	856.5	33.5	2310	10	US-11-055-679-6	Sequence 6, Appl
44	842.5	32.9	2200	7	US-10-451-010-13	Sequence 13, Appl
45	838	32.8	2428	5	US-10-106-698-1947	Sequence 1947, Ap

ALIGNMENTS

RESULT 1

US-10-813-588-1

; Sequence 1, Application US/10813588

; Publication No. US20050053969A1

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides

; TITLE OF INVENTION: Encoding the Same

; FILE REFERENCE: LEX-0071-USA

; CURRENT APPLICATION NUMBER: US/10/813,588

; CURRENT FILING DATE: 2004-03-30

; PRIOR APPLICATION NUMBER: US/09/691,344

; PRIOR FILING DATE: 2000-10-18

; PRIOR APPLICATION NUMBER: US 60/160,285

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/183,583

; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1464

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-813-588-1

Alignment Scores:

Pred. No.: 1,47e-292 Length: 1464
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-813-588-2 (1-487) x US-10-813-588-1 (1-1464)

QY	1	MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle	20
DB	1	ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACTCTTTGGGAAAGACAAAT	60
QY	21	ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	61	ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGAGATTTGGATATCGAATCCCGAG	120
QY	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys	60
DB	121	ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAGATCAATATGGTCCCATCTGT	180
QY	61	GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
DB	181	GGAAGTATGACTGTTCCCAAGAACTCTTGTGACACAACTGAGTAACCGTCCGCTTT	240
QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	241	GAGAGTGGATCCACATTTCTGGCGGGGTTTTTGTGACCTATGCGAGCAGCGACCAT	300
QY	101	ProAspLeuThrCysLeuGluLeuLeuAlaSerHisTyrLeuLysThrGluTyrSerLys	120
DB	301	CCAGATTTAATACATGTTTGGAAAGAGCTTAGCCATTTATTTGAAGACAGAAATACAGCAA	360
QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
DB	361	TTCTGCCAGCTGGTTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA	420
QY	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu	160
DB	421	TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGAGGAATATTTGCTGTAA	480
QY	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyLeu	180
DB	481	CTAGGTGGCCAGATCAGTGTGCTTCCAGCGAAAGGATCAGTCGATATGAAGGATCTG	540
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	541	GCCAAATGGTGTCTTTTCAGGGATGGTTCCCTGTGCACAAAGCGATTTCTGTTACCTCC	600
QY	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	601	AATGGTTGCAGCAGATCCTTGGATTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCCTCA	660
QY	221	TrpGlnSerValLeuGluSerGlyAspGluValHisTrpSerProGlyGlnAlaAspLeu	240
DB	661	TGGCAGTCGGTCAATGAGTGGAGACCAAGTTCACCTGCTCTCTGCGCAAGCCCGACTT	720
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerSerAsnHisLysProArgGlu	260
DB	721	CAGGACCAAGGCCCATCATGCGCTTCGGCGGACAGTAGCAACACCAACCCAGAGAG	780
QY	261	TrpLeuGluLeuAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer	280
DB	781	TGGCTGGAGATCGATTTTGGGGAGAAAAAATAACAGGAATTAGGACCAACAGGATCT	840
QY	281	ThrGlnSerAsnHisPheThrValLysSerPheValMetAsnHisLysAsnAsn	300
DB	841	ACACAGTCGAACCTTCAACTTTATGTTAAGAGTTTGTGATGAACCTTCAAAACCAATAT	900
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
DB	901	TCTAAGTGAAGACCTATAAGGAATTTGTAATTAAGAAAAAGGTGTTTCAGGGTAAC	960

321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
 961 TCTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCTCCCTCCCATCGTGCAGATATGT 1020
 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
 1021 CGGGTTGTCGCCAGACATGGCCAGAGAGTAGCTTGAAGGTGGAGCTCATTTGGTTGC 1080
 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
 1081 CAGATTACAAAGGTAATGATTCTTGGTGTGGCGCAAGCAAGTCAAAGCACCAGTGT 1140
 381 SerThrLysGlyGluAspGluThrIleThrArgProIleProSerSerGluThrSerThr 400
 1141 TCAACTTAAAGAAAGAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValValLeuValPheAla 420
 1201 GGATTAACAATTAACAAGGTGGCTATTCATTTGGTGCTCTCTTGTGCTGGTGTGCT 1260
 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
 1261 GGAATGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
 1321 GCGGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTCGACACATCAG 1380
 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
 1381 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGAGATGACACAAAAAGTTAGATCTC 1440
 481 IleThrSerAspMetAlaGly 487
 1441 ATCACAAGTGATATGGCAGT 1461

RESULT 2
 US-10-813-588-5
 ; Sequence 5, Application US/10813588
 ; Publication No. US20050053969A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
 ; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: LEX-0071-USA
 ; CURRENT APPLICATION NUMBER: US/10/813,588
 ; CURRENT FILING DATE: 2004-03-30
 ; PRIOR APPLICATION NUMBER: US/09/691,344
 ; PRIOR FILING DATE: 2000-10-18
 ; PRIOR APPLICATION NUMBER: US 60/160,285
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: US 60/183,583
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1620
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-813-588-5

Alignment Scores: 1,73e-292 Length: 1620
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-813-588-2 (1-487) x US-10-813-588-5 (1-1620)

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DB 217 ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGGAGATTGGATATCGATATCCAG 276
QY 41 ThrCysAlaSerAspTyrIleLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 277 ACCGTGCTTCTGACTATCTCTTCCACGAGCTCTCAGATCAATATGCTCCATCTGT 336
QY 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 337 GGAAGTATGACTGTCTCCCAAGAACTCTTGTGAAACAGTGAAGTAAACCGTCCGCTTT 396
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 397 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTCTGACCTATCGAGCAGCGACCAT 456
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerLys 120
DB 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATGAACACAGATACAGCAAA 516
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 517 TTCTGCCACGCTGTTGTAGACGCTGAGCAGGAGACATTTCTGGGAATATGGTAGTGA 576
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 577 TATAGATACCTCTTATTTGCAAGCTGCCATCCATCGAGGAATATTTGCTGATGAA 636
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTCTTACGCCAAGGGATCAGTCGATATGAAGGATTCGT 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuThrSer 200
DB 697 GCCAATGGTGTCTTTTCGAGGATGTTCCCTGTCCAGCAAGCGATTTCTGTGTACCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 757 ATGGTTGACGAGATCCTTGAGTTTGAACCTGCGGCAATATCAGACTTCTTCTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCTGGCCCAAGCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGGCTTGGGCGCAGTAGCAACCAACCAACCAACGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGlySer 280
DB 937 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATACAGGAATTAGGACCAAGATCT 996
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 997 ACACAGTCAACTTCAACTTTTATGTTAAGAGTTTTTGTGATGACTTCAAAACAATAAT 1056
QY 301 SerLysTrpLysThrTyrIysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAGGGTAA 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1117 TCTAATCTTCGGACCCAGTGAACAATTTCACTCCCTCCCATCGTGCCAGATATGG 1176
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360

DB 1177 CGGGTTGTCCCCAGACATGGCACCAGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTGC 1236
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGACAAGTCAAAAGCACCACTGTT 1296
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCACTTAAGAAAGAGTAGAGCAATCACAGGCCCATCCCTCCGGAAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
DB 1357 GCAATAAACAATTTACAACGGTGGCTATTCATTTGGTGTCTCTTGTCTGGTGTGTTGCT 1416
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysGlySerProTyrGlySer 440
DB 1417 GGAATGGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1476
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1477 GCGGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1537 TCAGCTGAGTTTACCATCAGCTATGATATATGAGAGGAGATGACACAAAAGTTAGATCTC 1596
QY 481 IleThrSerAspMetAlaGly 487
DB 1597 ATCACAAGTGATATGGCAGGT 1617

RESULT 3
US-10-295-027-1083
; Sequence 1083, Application US/10295027
; Publication NO. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1083
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1083

Alignment Scores:
  Pred. No.: 1,97e-292      Length: 1761
  Score: 2557.00           Matches: 487
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 100.00%      Indels: 0
  DB: 6                      Gaps: 0

US-10-813-588-2 (1-487) x US-10-295-027-1083 (1-1761)

QY 1 MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluYserThrIle 20
DB 298 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT 357
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 417
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 418 ACCTGAGCTTCTGACTATCTCTCTTCCAGGCTCTTCAGATCAATATGTCATACTGT 477
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuValArgPhe 80
DB 478 GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAACACAAAGTAGTAACCGTCCGCTTT 537
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 538 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGACCTATGCGAGCAGGACCAT 597
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIleYserThrGluTyrSerLys 120
DB 598 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 657
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 658 TTTCTGCCACCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 717
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 718 TATAGAGATACCTTTTATTGTGCAAGCTGCCATCCATCAGGAATAATTGCTGATGA 777
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 778 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGGATCAGTCGATATGAAGGGATTCTG 837
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DB 838 GCCAATGGTGTCTTTTCAGGGATGTTCTCTGTGACAGCAAGCAATTCGTTTACCTCC 897
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 898 AATGGTTGCAGCAGATCTCTTGAGTTTTTGAACCTGACGGCAATACAGAGCTTCTTCTCA 957
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 958 TGGCAGTCGCTCAATGAGTGGAGACCAAGTTTCACTGCTCTCTGCGCCAAAGCCGCACTT 1017
QY 241 GluAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 1018 CAGGACCAAGCCCATCATGGCTTTCGGGCGACAGTAGCAACAACCAACCAACAGAG 1077
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1078 TGGCTGAGATCGATTTGGGGGAAAAAAGAAATAACAGGAATTAGGACCCACAGGATCT 1137
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300

; SEQ ID NO 1197
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1083

1138 ACACAGTCGAACCTTCAACTTTTATGTATAGAGTTTTTGTGATGAACCTTCAAAACCAATAAT 1197
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
DB 1198 TCTAAGTGGAGACCTTATNAAGGATTTGTGATATATGAAGAAAGGTGTTTTCAGGGTAAC 1257
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1258 TCTAATCTTCCGGGACCCAGTCGCAAAACAATTTTATCCCTCCCATCGTGCCAGATATGTG 1317
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1318 CGGGTTGTCCCCAGACATGGCACCAGAGATAGCTTGAAGGTGAGCTCATTTGGTTGC 1377
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1378 CAGATTACACAGGTATATGATTCATTTGTTGGTGGCGCAAGCAAGTCAAGACCACTGTT 1437
QY 381 SerThrLysGlyLeuAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1438 TCAACTTAAAGAAAGATGAGACAATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1497
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
DB 1498 GGAATAAACATTACACCGGTGGCTATTCATTTGGTGTCTCTTGTCTGTGTTGCT 1557
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
DB 1558 GGAATGGGATCTTTGCAGCCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1617
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTrpPheAlaArgHisGln 460
DB 1618 GCAGAGCTTCAGAAAAACAGACTGTTGGAAGCAGATTAATAATATCCCTTTGCGACATCAG 1677
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1678 TCAGCTGAGTTTACCATCAGCTATGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1737
QY 481 IleThrSerAspMetAlaGly 487
DB 1738 ATCACAAGTGATATGCGAGT 1758

RESULT 4
US-10-813-588-3
; Sequence 3, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-3
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Alignment Scores:

Pred. No.: 1,97e-292 Length: 1761
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-813-588-2 (1-487) x US-10-813-588-3 (1-1761)

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QY 1 MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluIysThrIle 20
DB 298 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTGTCGGAAGACAAAT 357
QY 21 ThrValProIysGlyIysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCGAG 417
QY 41 ThrCysAlaSerAspTyrIleuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 418 ACCTGTGCTTCTGACTATCTCTCTCACAGCTCTTCAGATCAATATGGTCCATCTGT 477
QY 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 478 GGAAGTATGACTGTTCCTCAAGAACTCTTGTGAAACAAGTGAAGTAAACCGTCCGCTT 537
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 538 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTCTGACCTATCGGAGCAGCGACCAT 597
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerIys 120
DB 598 CCAGATTTAATACATGTTTGGAAACGAGCTAGGCATTATTTGAAGACACAAATACAGCAA 657
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 658 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 717
QY 141 TyrArgAspThrSerLeuLeuCysIysAlaAlaIleHisAlaGlyIleAlaAspGlu 160
DB 718 TATAGATACCTCTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTTCTGATGAA 777
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgIysGlyIleSerArgTyrGluGlyIleLeu 180
DB 778 CTAGGTGGCCAGATCAGTGTCTTACGCCAAGGGATCAGTCGATATCAAGGGATTCTG 837
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspIysArgPheLeuPheThrSer 200
DB 838 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTTCAGACAAGCGATTTCTGTTTACCTCC 897
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 898 AATGTTGGACGAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCCTCA 957
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 958 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTCGGCCAAGCCGACTT 1017
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisIysProArgGlu 260
DB 1018 CAGGACCAAGGCCCATCATGGGCTTGGGGCGACAGTAGCAACAACCAACCAACGAGAG 1077
QY 261 TrpLeuGluIleAspLeuGlyGlyIysIysIleThrGlyIleArgThrThrGlySer 280
DB 1078 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAAATACAGGAATTAGGACCAAGATCT 1137
QY 281 ThrGlnSerAsnPheAsnPheTyrValIysSerPheValMetAsnPhelysAsnAsn 300
DB 1138 ACACAGTGGAACTCAACTTTTATGTTAAGAGTTTGTGATGACTTCAAAACCAATAAT 1197
QY 301 SerIysTrpIysThrTyrIysGlyIleValAsnAsnGluGlyIysValPheGlnGlyAsn 320
DB 1198 TCTAAGTGGAGACCTATAAGAAATTTGTGAATAATGAAGAAAAAGGTGTTTCAGGGTAAC 1257
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QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1258 TCTAATCTTTCGGACCCAGTGCAAAACAATTTTCATCCCTCCCATCGGCCAGATATGTG 1317
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuIysValGluLeuIleGlyCys 360
DB 1318 CGGGTTGTCCCCGACACATGGCAGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1377
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1378 CAGATTACAAAGGTAATGATTTCATTTGGTGTGGCCGACAGCAAGTCAAAAGCACCACTGT 1437
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1438 TCACACTAGAAAGAGATGAGACATCACAGGCCCATCCCTCGGAAGAAATCATCCACA 1497
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
DB 1498 GGAATAAAACATTTACAAACGGTGGCTATTCATTTGGTGTCTCTTGTGTTCTCTGGTGTGCT 1557
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysIysLysLysLysGlySerProTyrGlySer 440
DB 1558 GGAATGGGGATCTTTGCAGCCTTTAGAAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1617
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1618 GCGGAGGCTCAGAAAACAGACTGTTGGAGACAGATTAATATATCCCTTTCCAGACATCAG 1677
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluIysGluMetThrGlnLysLeuAspLeu 480
DB 1678 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1737
QY 481 IleThrSerAspMetAlaGly 487
DB 1738 ATCACAAAGTATATGGCAGGT 1758
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RESULT 5
US-10-813-588-7
; Sequence 7, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; PRIOR FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-7

Alignment Scores:
Pred. No.: 1,99e-292 Length: 1768
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1082

; LENGTH: 2010

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-295-027-1082

Alignment Scores:

Pred. No.:	2,446-292	Length:	2010
Score:	2557.00	Matches:	487
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-813-588-2 (1-487) x US-10-295-027-1082 (1-2010)

QY	1	MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle	20
DB	282	ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTGTCGAAAGACAATT	341
QY	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	342	ACAGTACCAAGGGAAAGACTGATCTGAGGTTGGAGATTGGATATCGAATCCCAAG	401
QY	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys	60
DB	402	ACCTGTGCTTCTGACTATCTCTCTTACCAGCTCTTTCAGATCAATATGTCCTACTGT	461
QY	61	GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
DB	462	GGAAATGATGACTGTTCCCAAGAACTCTTGTGTAACACAAAGTGAAGTAAACCGTCGCTTT	521
QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	522	GAGATGGGATCCACATTTCTGCGCGGGTTTTTGTGCTACCTATGCGAGCAGCCACAT	581
QY	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
DB	582	CCAGATTTAATACATGTTTGGACGAGCTAGCCATTAATTCAGACAGATACAGCAAA	641
QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
DB	642	TTCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGCTAGTGA	701
QY	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu	160
DB	702	TATAGATATACCTCTTTATTTGCAAAAGCTGCCATCCATGCGAGGAATAATTGCTGAT	761
QY	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
DB	762	CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATCTG	821
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	822	GCCAAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAAAGCAATTTCTGTTACCTCC	881
QY	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	882	AATGGTTGCAGAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCCCTCA	941
QY	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
DB	942	TGGCAGTCCGTCATGAGATGGAGACCAAGTTCACTGTCTCTGCGCAACCCGACTT	1001
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu	260
DB	1002	CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACAACCAACCAACGAGAG	1061
QY	261	TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer	280
DB	1062	TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCACGAGATCT	1121

QY	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn	300
DB	1122	ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTTGATGACTTCAAAACATATAT	1181
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
DB	1182	TCTAAGTGAAGACCTATAAAGGAATTGTGAATAATAGAGAAAGGTGTTTCAGGGTAAC	1241
QY	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340
DB	1242	TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCCATCGTGCCAGATATG	1301
QY	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys	360
DB	1302	CGGGTTGTCCTCCACACATGGCCACAGAGATAGCTTGAAGGTGGAGCTCATTTGGTTGC	1361
QY	361	GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal	380
DB	1362	CAGATTACAAAGGTAATGATTCAATTGTTGTGGCGCAAGACAAGTCAAAAGCACCACTGT	1421
QY	381	SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr	400
DB	1422	TCACTAAGAAAGAAGATGAGACAATCAAGGCCCATCCCTCGAAGAAACATCCACA	1481
QY	401	GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla	420
DB	1482	GGAAATAACATTTACAACGGTGGCTATTTCATTGGTGTCTCTTGTGCTCTGCTGTTGCT	1541
QY	421	GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys	440
DB	1542	CGAATGGGGATCTTTGACGCTTTAGAAAAGAGAAAGAAAGAAAGTCCGTATGGATCA	1601
QY	441	AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln	460
DB	1602	GCAGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG	1661
QY	461	SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu	480
DB	1662	TCAGCTGATTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAAGTTAGATCTC	1721
QY	481	IleThrSerAspMetAlaGly	487
DB	1722	ATCACAGTGATATGGCAGGT	1742

RESULT 7

US-10-783-528-23

; Sequence 23, Application US/10783528

; Publication No. US20040219579A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Gish, Kurt

; APPLICANT: Wilson, Keith

; APPLICANT: Zlotnick, Albert

; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND

; FILE REFERENCE: 05882.0191.NPUS01

; CURRENT APPLICATION NUMBER: US/10/783, 528

; CURRENT FILING DATE: 2004-02-19

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 23

; LENGTH: 2010

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-783-528-23

Alignment Scores:

Pred. No.:	2,446-292	Length:	2010
Score:	2557.00	Matches:	487
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-813-588-2 (1-487) x US-10-783-528-23 (1-2010)

QY 1 MetThrSerIysAsnThrProGlyThrTyrProAsnHisThrValCysGluIysThrIle 20
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|
Db 282 ATGACATCTAAGAAATATCCGGGACCTACCCCAATCACACTGTTTGGGAAAAGACAAAT 341
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|
|
QY 21 ThrValProIysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
|
|
|
Db 342 ACAGTACCAAGGGGAAAAGACTGATCTCGAGTTGGGAGATTGGATATCGAATCCCGAG 401
|
|
|
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
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|
|
Db 402 ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAGATCAATATGGTCCATCTGT 461
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|
|
QY 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
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|
|
Db 462 GGAAGTATGACTGTTCCCAAGAAGACTCTTGTTCACACACAACTAAGTAAACCGTCCGCTTT 521
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|
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
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|
|
Db 522 GAGAGTGGATCCACACATTTCTGGCCGGGGTTTTTGTGACCTATTCGAGCAGCGACCAT 581
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|
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerLys 120
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|
Db 582 CCAGATTATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGATACAGCAA 641
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|
|
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
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|
Db 642 TTCCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 701
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|
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisIleLeuLeuLeuAspGlu 160
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Db 702 TATAGAGATACCTCTTTATTGTGCAAGCTGCATCATCATGACAGAAATAATTGCTGATGAA 761
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QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
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|
Db 762 CTAGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAGGGATCTCG 821
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|
|
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
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Db 822 GCCAATGGTGTCTTTCCGAGGATGGTTCTCCTGTCCAGACAAGCGATTTCTGTTTACTCC 881
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|
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
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|
Db 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGCAGCGCAATTCAGAGCTTCTTCTCTCA 941
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|
|
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
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|
Db 942 TGGCAGTGGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTTGGCCAAAGCCGACTT 1001
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QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnHisLysProArgGlu 260
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Db 1002 CAGGACCAAGGCCCATCATGGCTTCGGCGCACAGTAGCAACAACCAACCAACGAGAG 1061
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|
QY 261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer 280
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|
|
Db 1062 TGGCTGGAGATCGAATTTGGGGGAAAAGAAAATAACAGGAATTTAGGACACAGGATCT 1121
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|
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
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Db 1122 ACAGTTCGAACTCACTTTATATGTTAAGATTGTTGTGATGAATTCAAAACCAATAAT 1181
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|
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
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|
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Db 1182 TCTAAGTGAAGACCTATAAGGAATTTGTGAATAATGAAGAAAAGGTGTTTCAGGGTAAC 1241
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|
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
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Db 1242 TCTAATCTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1301
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|
QY 341 ArgValValProGlnThrTrpHisGlnAlaArgIleAlaLeuLysValGluLeuIleGlyCys 360
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|
Db 1302 CGGGTTGTCCCCCAGACATGGCACCCAGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1361
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QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
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|
Db 1362 CAGATTTACACAAGGTAAATGATTCATTTGGTGGCGCAAGACAAGTCAAAAGCACCAAGTGT 1421
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|
|
QY 381 SerThrLysLeuGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
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|
|
Db 1422 TCACCTAAGAAAGAGATGAGCAATCAAGGCCATCCCCCTCGAAGAAACATCCACA 1481
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|
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
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|
|
Db 1482 GGAATAAACATTTACAACGGTGGCTATTCATTGGTGCTCTTGTGCTGGTGTGCT 1541
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QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysGlySerProTyrGlySer 440
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Db 1542 GGAATGGGGATCTTTTCAGACCTTTAGAAAGAAAGAAAGAAAGGAAGTCCGTATGGATCA 1601
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QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
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Db 1602 GCAGAGGCTCAGAAAACAGACTGTTGGAAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1661
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QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
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Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGGAGATGACACAAAAGTTAGATCTC 1721
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QY 481 IleThrSerAspMetAlaGly 487
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Db 1722 ATCACAAGTGATATGGCAGGT 1742
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|
|
RESULT 8
US-10-783-528-24
; Sequence 24, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-783-528-24

Alignment Scores:
Pred. No.: 2,44e-292 Length: 2010
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-813-588-2 (1-487) x US-10-783-528-24 (1-2010)

QY 1 MetThrSerIysAsnThrProGlyThrTyrProAsnHisThrValCysGluIysThrIle 20
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Db 282 ATGACATCTAAGAAATATCCGGGACCTACCCCAATCACACTGTTTGGGAAAAGACAAAT 341
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QY 21 ThrValProIysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
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Db 342 ACAGTACCAAGGGGAAAAGACTGATCTCGAGTTGGGAGATTGGATATCGAATCCCGAG 401
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QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
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Db 402 ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAGATCAATATGGTCCATCTGT 461
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QY 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
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Db 462 GGAAGTATGACTGTTCCCAAGAAGACTCTTGTTCACACACAACTAAGTAAACCGTCCGCTTT 521
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QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
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Db 522 GAGAGTGGATCCACACATTTCTGGCCGGGGTTTTTGTGACCTATTCGAGCAGCGACCAT 581
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QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
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QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisIleLeuLeuLeuAspGlu 160
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QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
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Db 762 CTAGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAGGGATCTCG 821
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QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
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Db 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGCAGCGCAATTCAGAGCTTCTTCTCTCA 941
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QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
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QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
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Db 1362 CAGATTTACACAAGGTAAATGATTCATTTGGTGGCGCAAGACAAGTCAAAAGCACCAAGTGT 1421
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QY 381 SerThrLysLeuGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
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Db 1422 TCACCTAAGAAAGAGATGAGCAATCAAGGCCATCCCCCTCGAAGAAACATCCACA 1481
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QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
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Db 1482 GGAATAAACATTTACAACGGTGGCTATTCATTGGTGCTCTTGTGCTGGTGTGCT 1541
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QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysGlySerProTyrGlySer 440
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Db 1542 GGAATGGGGATCTTTTCAGACCTTTAGAAAGAAAGAAAGAAAGGAAGTCCGTATGGATCA 1601
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QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
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QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
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Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGGAGATGACACAAAAGTTAGATCTC 1721
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QY 481 IleThrSerAspMetAlaGly 487
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Db 1722 ATCACAAGTGATATGGCAGGT 1742
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RESULT 8
US-10-783-528-24
; Sequence 24, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-783-528-24

Db 462 GGAAGTATGACTCTTCCCAAGAACTCTTGTGAACACAACTGAAGTAAACCGTCCGCTTT 521
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyraIaSerSerAspHis 100
Db 522 GAGAGTGGATCCCACTTTCTGCCCGGGTTTTTGTGACCTATCGAGCAGCGACCAT 581
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyraIeLeuLysThrGluTyraSerLys 120
Db 582 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTGAAGACAGAAATACAGCAA 641
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 642 TTCGTGCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 701
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 702 TATAGAGATACCTCTTTATTTGTCAAGCTGCCATCCATGCGAGGAATAATTGCTGATGAA 761
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyraGluGlyIleLeu 180
Db 762 CTAGGTGGCCAGATCAGTGTCTTCAGCGCAAGGGATCAGTCGATAGGGATTCTG 821
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
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QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 882 AATGGTGTGACAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCCCTCA 941
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 942 TGGCAGTGGTCAATCAGAGTGGAGACCAAGTTCACTGTCTCTGTCGCAAGCCGACTT 1001
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 1002 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAACAGAG 1061
QY 261 TrpLeuGluIleAspLeuGlyGlyLysValIleThrGlyIleArgThrThrGlySer 280
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATAACAGGAATTAGGACCAAGATCT 1121
QY 281 ThrGlnSerAsnPheAsnPheTyraValLysSerPheValMetAsnPhelLysAsnAsn 300
Db 1122 ACACAGTCGACTCACTTTATGTTAAGATTTTGTGATGACTTCAAAACCAATAT 1181
QY 301 SerLysTrpLysThrTyraLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 1182 TCTAAGTGAAGACCTATAAGGAATTTGTAATATGAAGAAAGGTGTTTCAGGGTAAC 1241
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyraVal 340
Db 1242 TCTAACTTTGGGACCCAGTCGAAACAATTTTCATCCCTCCCATCGTGCCAGATATG 1301
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1302 CGGGTGTCTCCCGACAGATGGCAGAGATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1361
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1362 CAGATTACAAAGGTAATGATTCATTTGTTGGCGCAGACAAAGTCMAAGCACCAGTGT 1421
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluLysThrSerThr 400
Db 1422 TCAACTTAAGAAAGAGATGAGACAAATCAGAGGCCCATCCCTCGGAAGAAATCCACA 1481
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValPheAla 420
Db 1482 GGAATAAACAATTACACGGTGGCTATTCCATTGGTGTCTCTTGTGTCCTGGTGTGCT 1541
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440

Db 1542 GGAATGGGACTTTTGCAGCCTTTAGAAAAGAAAGAAAGAGTCCGTATGGATCA 1601
QY 441 AlaGluAlaGlyThrAspCysTrpLysGlnIleLysTyraPheAlaArgHisGln 460
Db 1602 GCAGAGGCTCAAGAAACAGACTGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1661
QY 461 SerAlaGluPheThrIleSerTyraAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGGAGATGACACAAAAGTTAGATCTC 1721
QY 481 IleThrSerAspMetAlaGly 487
Db 1722 ATCACAAGTGATATGCGAGGT 1742

RESULT 9

US-09-759-130B-72
; Sequence 72, Application US/09759130B
; Publication NO. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-130B-72

Alignment Scores:
Pred. No.: 1,396-291 Length: 2145
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 3 Gaps: 0

US-10-813-588-2 (1-487) x US-09-759-130B-72 (1-2145)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 157 ATGACATCTAAGAAATTTATCCGGGAGCTACCCCAATCACACTGTTTGGGAAAAGACAAT 216
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 217 ACAGTACCAAGGGGAAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCGAG 276
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 277 ACCTGTGCTCTGACTATCTCTCTTCCAGGCTCTTCAGATCATATGTCCTACTGTT 336
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 337 GGAAGTATGACTGTTCCCAAGAAGCTTGTGTGAACACAAAGTCAAGTAAACCGTCCGCTTT 396
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 397 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTGCTGACCTATCGAGCAGCGACCAT 456
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 457 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACGAAA 516
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 517 TTCTGCCAGCTGGTTGTAGAGAGCTAGCAGGAGACATTTCTCGGAATATGGTAGATGA 576
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu 160
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QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGATCTG 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 697 GCCAATGGTGTCTTTCAGGGATGGTTCCCTGTGACACAAGCGATTTCTGTTCCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 757 AATGGTTGACAGCATCTTGTAGTTTTTGAACCTGACGGCAAAATCAGAGCTTCTTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTTCGTTCATGAGAGTGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACCTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGTAGCAACAACCAACCAACAGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyLysArgLysValIleThrGlyIleArgThrThrGlySer 280
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QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
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QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGAAGACCTATAAGGAATTTGTAATAATGAAGAAAGGTTTTCAGGGTAA 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
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QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1177 CGGGTTGTCCCCAGACATGGCACGAGAGATAGCTTTGAAGTTGGAGCTCATTTGTTGC 1236

QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTACACAAGGTAATGATTCAATGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1296
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCAACTAAGAAAAGAGATGAGACAATCAAGGCCCATCCCTCGAAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
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QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
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QY 481 IleThrSerAspMetAla 486
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US-10-741-790-72
; Sequence 72, Application US/10741790
; Publication NO. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NNIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-790-72

Alignment Scores:

Pred. No.: 1-39e-291 Length: 2145
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 7 Gaps: 0

US-10-813-588-2 (1-487) x US-10-741-790-72 (1-2145)

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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 157 ATGACATCTAAGAAATATATCCGGACCTACCCCAATCACACTGTGTTGCGAAAGACAAAT 216
QY 21 ThrValProGlyGlyArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 217 ACAGTACCAAGAGGAGAAAGAGCTGATCTCGAGGTTGGAGATTGGATATCGAATCCCGAG 276
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 277 ACTGTGCTCTGACTATCTCTTCACACGCTCTTCAGTCAATATGCTCATACTGT 336
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 337 GGAAGTATGACTGTTCCTCCCAAGAACTCTTGTGTAACACAACTGAGTAACTGCGCTTT 396
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 397 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTCTGCTACCTATGCGAGCGAGCCAT 456
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 457 CCAGATTATTAACATGTTTGGNACGAGCTAGCCATTATTTGAGNACAGNATACAGCAA 516
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 517 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGCTAGTGA 576
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 577 TATAGATATACCTCTTTATTGTGCAAGCTGCCATCCATGCGAGGAATAATTGCTGATGA 636
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAGGGATCTG 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 697 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGACGATTTCTGTTTACCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
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QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTyrProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTGGTCAATGAGAGTGGAGCCAAAGTTCACTGGTCTCTCGGCCCAACCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGCAGTAGCAACAAACACAAACCCAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer 280
DB 937 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAATACAGGAATTAGGACCAACAGGATCT 996
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QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 997 ACACAGTCGAACCTTCACTTTTATGTTAAGATTGTTGATGAACCTTCAAAACAATAAT 1056
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGGAGACCTATATAAGGAATTTGTAATATGAAGAAAGGTGTTTCAGGGTAAC 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1117 TCTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCCATCGTGCCAGATATGTG 1176
QY 341 ArgValValProGlnThrTyrHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1177 CGGGTTGTCCTCCACAGCATGGCCAGAGATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1236
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTyrArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCAGTGT 1296
QY 381 SerThrLysGlyGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCAACTAAGAAAGAGATGAGACAATCAAGAGCCCATCCCTCGGAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
DB 1357 GGAATTAACATTTACAAAGGTGGCTATTCATTTGGTGTCTCTTGTGCTCGTGGTTGCT 1416
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
DB 1417 GGAATGGGATCTTTGCGAGCCTTTAGAAAGAAAGAGAGAAAGAAAGTCCGTATGGATCA 1476
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1477 GCAGAGGCTCGAANAACAGACTGTTGGAAGCAGATTAATATATATATATATATATATAT 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1537 TCAGCTGAGTTTACCATTACCTAGCTATGATATGAAAGGAGATGACACAAAGATTAGATCTC 1596
QY 481 IleThrSerAspMetAla 486
DB 1597 ATCAAGTGTATGGCA 1614
RESULT 11
US-10-312-352-47
; Sequence 47, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: HE, Ann; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Danniell B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURFORD, Neil; YAO, Monique G.
; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
; APPLICANT: BAUGHN, Mariah R.; HAPALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROMSKY, Mark L.
; APPLICANT: LU, Dying Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
; APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PP-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/21067
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/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215,454
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 60/219,462
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: US 60/240,111
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: US 60/240,106
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: US 60/244,021
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: US 60/248,887
/ PRIOR FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: US 60/249,570
/ PRIOR FILING DATE: 2000-11-16
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PERL Program
/ SEQ ID NO 47
/ LENGTH: 2888
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20040053824A1 184661CBI
US-10-312-352-47

Alignment Scores:
Pred. No.: 2,24e-291 Length: 2888
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 7 Gaps: 0

US-10-813-588-2 (1-487) x US-10-312-352-47 (1-2888)

QY 1 MetThrSerLysAlaThrProGlyThrTyProAsnHisThrValCysGluLysThrIle 20
Db 282 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTTCGGAAGACAAAT 341
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyValAspLeuAspLeuGln 40
Db 342 ACAGTACCAAGGGGAAAGACTGATCTCGAGTTGGGAGATTTGATATCGAATCCAG 401
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
Db 402 ACCTGTGCTTCTGACTATCTCTCTTCCACGAGCTCTTCAGATCAATATGTCATCTGT 461
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 462 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAACACAAAGTGAAGTAACCGTCCGCTTT 521
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 522 GAGAGTGATGCCACATTTCTGCGCGGGTTTTTGTCTGACCTATGCGACACGACCAT 581
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 582 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATTTATTGAAGACAGAAATACAGCAA 641
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 642 TTTCTGCCACCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 701
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 702 TATAGATATACCTTTTATTGTGCAAGCTGCCATCCATGAGGAATATGCTGATGAA 761
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 762 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGGATCAGTCGATATGAAGGATTCGT 821
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
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Db 822 GCCAATGGTGTCTTTCCAGGAGATGTTCCCTGTGAGCAAGCGATTTCTGTTTACCTCC 881
QY 201 AenGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 941
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 942 TGGCAGTCCGTCAATCAGAGTGGAGCAAGTTCATGCTGCTCTCTGGCCAAAGCCGACTT 1001
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 1002 CAGGACCAAGGCCCATCATGGCTTCGGGCGCAGTAGCAACACCAACACCAAGAG 1061
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrGlySer 280
Db 1062 TGGCTGGAGTCGATTTGGGGAGAAAAGAAAATAACAGGAATTTAGGACCACAGATCT 1121
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 1122 ACACAGTCCAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATA 1181
QY 301 SerLysTrpLysThrTyrLysGlyIleValLeuAsnGluGluLysValPheGlnGly 320
Db 1182 TCTAAGTGGAGACCTATAAGAAATTTGAAATAATGAAGAAAGTGTTCAGGGTAAC 1241
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
Db 1242 TCTAACTTTCCGGACCCAGTCGAAACAATTTTCATCCCTCCCATCGTGCCAGATATGT 1301
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1302 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCCTTGAAGGTGGAGTCTATTGGTTGC 1361
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1362 CAGATTACCAAGGTAATGATTCATTTGGTGGCGCAAGCAAGTCNAAGCCAGTGT 1421
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1422 TCAACTAAGAAAGAGATGAGACAATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1481
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
Db 1482 GGAATAAACAATTACACCGTGGCTATTCATTTGGTGGTCTCTTTGTTGTCCTGGTGT 1541
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
Db 1542 GGAATGGGATCTTTGACGCCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1602 GCAGAGCTCAGAAAACACAGCTGTTGGAAGCAGATTTAAATATCCCTTCCGACATCAG 1661
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATGATAATGGAAGGAGATGACACAAAAGTTAGATCT 1721
QY 481 IleThrSerAspMetAla 486
Db 1722 ATCAACAAGTATATGGCA 1739

RESULT 12
US-10-003-132-1
; Sequence 1, Application US/10003132
; Publication No. US20020192750A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Gao, Zeren
; APPLICANT: Shoemaker, Kimberly E.
; TITLE OF INVENTION: NEUROFILIN HOMOLOG 2CUBS
; FILE REFERENCE: 00-62
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; CURRENT APPLICATION NUMBER: US/10/003,132
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,004
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76) ... (2223)
US-10-003-132-1

Alignment Scores:
Pred. No.: 2,58e-291 Length: 3151
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 5 Gaps: 0

US-10-813-588-2 (1-487) x US-10-003-132-1 (1-3151)

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QY      1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB      232 ATGACATCTAAGATTATCCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAA 291

QY      21 ThrValProLysGlyLysArgIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB      292 ACAGTACCAGGAGGAAAGACTGATTCTGAGCTGGGAGATTGGCATATCGAATCCAG 351

QY      41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB      352 ACCGTGCTCTCGACTATCTCTTCACAGCTCTTCAGATCAATATGGTCCACTACTGT 411

QY      61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB      412 GGAAGTATGACTGTTCCCAAGACTCTGTTGMAACACAGTGAAGTAACCGTCGCTTT 471

QY      81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB      472 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTCTGACCTATCGAGCAGCAGCACCAT 531

QY      101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB      532 CCAGATTTAATAACATGTTTGGACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 591

QY      121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB      592 TTCCTGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGATGATGA 651

QY      141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB      652 TATAGAGATACCTCTTTATGTGTCAAGCTGCATCCATCGAGGAATAATTGCTGATGAA 711

QY      161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB      712 CTAGGTGGCCAGATCAGTGTGTTGAGCCAAAGGGGATCAGTCGATATGAAGGGATTCTG 771

QY      181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB      772 GCCAATGGTGTCTTTCGAGGATGGTTCCTGTCAGACAGCGATTCTGTTTACCTCC 831

QY      201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB      832 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTCTTCTCTCA 891

QY      221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB      892 TGGCAGTCGGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTTGGCCAGCCCGACTTT 951
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QY      241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB      952 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACACACCAACACACAGAG 1011

QY      261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB      1012 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCCACAGGATCT 1071

QY      281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValIleAsnPheLysAsnAsn 300
DB      1072 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAACAATAAT 1131

QY      301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB      1132 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1191

QY      321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB      1192 TCTAACTTTTCGGGAGCCAGTGCAGAAACAATTTTCATCCCTCCCATCGGCCAGATATGTG 1251

QY      341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB      1252 CGGGTTGTCCTCCCGACATGGCCAGAGGATAGCCCTTGAAGGTGGAGCTCAATTGGTTGC 1311

QY      361 GlnIleThrGlnGlnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB      1312 CAGATTACACAGGTAATGATTTTCATTTGGTGTGGCGCAGACAAAGTCAAGACCACTGTT 1371

QY      381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerSerGluThrSerThr 400
DB      1372 TCAACTAAGAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1431

QY      401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
DB      1432 GGAATAAACATTTACAAACGGTGGCTATTTCCATTTGGTGCTCTCTGTTCTCTGGTGTGCT 1491

QY      421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
DB      1492 GGAATGGGATCTTTGCAGCCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551

QY      441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB      1552 GCAGAGGCTCAGAAACACAGACTGTTTGAAGCAGAGATTAATAATATCCCTTTGCCAGACATCAG 1611

QY      461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB      1612 TCAGCTGAGTTTACCATCAGCTATGATTAATGAAGAGGAGATGACACAAAGTTAGATCTC 1671

QY      481 IleThrSerAspMetAla 486
DB      1672 ATCACAGTGATATGCA 1689

RESULT 13
US-09-759-1308-71
; Sequence 71, Application US/097591308
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NMIM
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/ CURRENT APPLICATION NUMBER: US 09/759,130B
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 71
/ LENGTH: 3594
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-759-130B-71

Alignment Scores:
Pred. No.: 3,18e-291 Length: 3594
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 3 Gaps: 0

US-10-813-588-2 (1-487) x US-09-759-130B-71 (1-3594)

QY 1 MetThrSerIleAspThrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 228 ATGACATCAATGAAGTATATCCCGGACCTACCCCAATCACACTGTTTCGGAAAGACAT 287
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 288 ACAGTACCAAGGGGAAAGACTGATTCTGAGGTTGGAGATTTCGATATCGAATCCAG 347
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 348 ACCTGTGCTTCTGACTATCTCTCTTCCAGGCTCTTCAGATCAATATGCTCCATCTGT 407
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValAspPhe 80
DB 408 GGAAGTATGACTGTTCCCAAGAACCTCTGTTGACACAGAGTAAACCGTCCGCTTT 467
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 468 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGACCTATCGAGCAGCGACCAT 527
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrIleLysThrGluTyrSerLys 120
DB 528 CCAGATTATATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 587
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 588 TTCTGCCCGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGAAATATGGTAGATGA 647
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu 160
DB 648 TATAGAGATACCTCTTTATTGTCGAAAGCTGCCATCCATCCAGGAATATATGCTGTAA 707
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180

DB 708 CTAGGTGCCAGATCAGTGTGCTTCAGCGCAAGGATCAGTCGATATGAAGGGATTCTG 767
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 768 GCCAATGGTGTCTTTCGAGGGATGTTCCCTGTGACACAGCGATTCTGTATTACCTCC 827
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 828 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCTCTCA 887
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 888 TGGCAGTCGGTCAATGAGAGTGGACCAAGTTCACTGTCTCTCCGCGCAAGCCGACTT 947
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 948 CAGGACCAAGGCCCATCATGGGCTTCGGGCGAGTAGCAACAACCAACCAACGAGAG 1007
QY 261 TrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1008 TGGCTGGAGATCGATTTGGGGGAGAAAATAACAGGAATTAGGACCAAGATCT 1067
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1068 ACAGATCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAACAATAAT 1127
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGlyLysValPheGlnGlyAsn 320
DB 1128 TCTAAGTGGAGACCTATAAAGGAATTTGTAATATGAAGAAAGGTGTTTCAGGGTAAC 1187
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1188 TCTAATCTTCGGGACCCAGTGCACAAACAATTTTCATCCCTCCATCGTGGCCAGATATGT 1247
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1248 CGGTTGTCCTCCACAGATGGCAGAGATAGGCTTGAAGTGGAGCTCATTTGGTTGC 1307
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1308 CAGATTACACAGGTAATGATTTTCATTTGGTGTGCGCAAGTCAAAAGCACCAGTGT 1367
QY 381 SerThrLysGlyGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1368 TCAACTTAAGAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1427
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
DB 1428 GGAATAAACATTTACACGGTGGCTATTTCCATTTGGTGCTCTTGTGTTCTGTGTTGCT 1487
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
DB 1488 GGAATGGGATCTTTGCAGCCCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1547
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1548 GCAGAGGCTCAGAAAAACAGACTGTTGGAAGACAGATTAAATATATCCCTTTCAGACATCAG 1607
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1608 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGAGAGATGACACAAAAGTTAGATCTC 1667
QY 481 IleThrSerAspMetAla 486
DB 1668 ATCACAAGTGATATGCCA 1685

RESULT 14

US-10-741-790-71
; Sequence 71, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.

```
/ APPLICANT: McCarthy, Sean A
/ APPLICANT: Fraser, Christopher C
/ APPLICANT: Sharp, John D
/ APPLICANT: Barnes, Thomas S
/ APPLICANT: Kirst, Susan J
/ APPLICANT: Mackay, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wrighton, Nicolas
/ APPLICANT: Goodearl, Andrew
/ APPLICANT: Holtzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ TITLE OF INVENTION: USES.
/ FILE REFERENCE: MPI00-5350NMIM
/ CURRENT APPLICATION NUMBER: US/10/741,790
/ PRIOR FILING DATE: 2003-12-19
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 71
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-741-790-71

Alignment Scores:
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Score: 2551.00 Matches: 486
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 7 Gaps: 0

US-10-813-588-2 (1-487) x US-10-741-790-71 (1-3594)

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Db 228 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGCAAGACAAAT 287
Qy 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db 288 ACAGTACCAAGGGGAAAGACTGATTCTCGAGTTGGGAGATTTCGATATCGAATCCCAAG 347
Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 348 ACCCTGTCTTCGACTATCTCTTCCACCACTCTTCAGATCAATATGGTCCATCTGTT 407
Qy 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 408 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGAACACAGTGAAGTAACTGCTGCTTT 467
Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
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468 GAGAGTGGATCCACATTTCTGCCGGGGTTTTTTGTCTGACCTATCGGAGCAGCGACCAT 527
101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
528 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCCATATTATTGAAGACAGATACACAAA 587
121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
588 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGAGAGCATTTCTGGGAATATGTTAGATGGA 647
141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
648 TATAGAGATACCTCTTTATTGTGCAAGCTGCATCCATCGAGGAATAATTGCTGATGAA 707
161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
708 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGAGGATCAGTCGATATGAAGGATTCGTG 767
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201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
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948 CAGGACCAAGGCCCATCATGGCTTCGGCGGACAGTAGCAACACACCAACACAGAGAG 1007
261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer 280
1008 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACACACAGATCT 1067
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301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
1128 TCTAAGTGGAGACCTATTAAGGAATTTGTAATATGAAGAAAGAGTGTTCAGGGTAAAC 1187
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381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
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QY 461 SerAlaGluPheThrIleSerTyrAspAenGluLysGluMetThrGlnLysLeuAepLeu 480
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QY 481 IleThrSerAspMetAla 486
 Db 1668 ATCACAAGTGATATGGCA 1685

RESULT 15

US-09-814-353-20367
 ; Sequence 20367, Application US/09814353
 ; Publication No. US20030165831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Pamela
 ; APPLICANT: Lillie, James
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
 ; FILE REFERENCE: MRI-006B
 ; CURRENT APPLICATION NUMBER: US/09/814,353
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US 60/191,031
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/207,124
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 60/211,940
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: US 60/216,820
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/220,661
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/257,672
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 22037
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 20367
 ; LENGTH: 3676
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 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 3676
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-814-353-20367

Alignment Scores:
 Pred. No.: 3,29e-291 Length: 3676
 Score: 2551.00 Matches: 486
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.77% Indels: 0
 DB: 3 Gaps: 0

US-10-813-588-2 (1-487) x US-09-814-353-20367 (1-3676)

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 QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAepIleGluSerGln 40
 Db 354 ACAGTACCAAGGGGAAAGACTGATCTCGAGGTTGGGAGATTTGGATATCGAATCCCGAG 413
 QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
 Db 414 ACCTGTGCTCTTGACTATCTCTCTCCACGAGCTCTTCAGATCAATATGATGCTACTACTGT 473
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuAenThrSerGluValThrValArgPhe 80
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QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerSerHis 100
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 QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
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 QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
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Search completed: January 15, 2006, 23:23:40
Job time : 981 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:11:17 ; Search time 7270 Seconds
(without alignments)

11446.879 Million cell updates/sec

Title: US-10-813-588-1

Perfect score: 1464

Sequence: 1 atgacatctaagaattatcc.....caagtgatggcaggttaa 1464

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

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10: gb_sts.*

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12: gb_un.*

13: gb_vi.*

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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1464	100.0	1464	6 AX118816	Sequence
3	1464	100.0	1620	6 AR542473	Sequence
4	1464	100.0	1620	6 AX118820	Sequence
5	1464	100.0	1761	6 AR542472	Sequence
6	1464	100.0	1761	6 AX118818	Sequence
7	1464	100.0	1768	6 AR542474	Sequence
8	1464	100.0	1768	6 AX118822	Sequence
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11	1462.4	99.9	2010	8 BC035671	Homo sapi
12	1459.8	99.7	2888	6 AX704743	Sequence
13	1459.8	99.7	3676	6 CO413296	Sequence
14	1440.2	98.4	2547	6 AX833875	Sequence
15	1440.2	98.4	2547	8 AK095973	Homo sapi
16	584.2	39.9	2473	6 CS034882	Sequence
17	584.2	39.9	2473	6 CS043834	Sequence
18	584.2	39.9	2473	6 AX835251	Sequence

ALIGNMENTS

RESULT 1

AR542471

LOCUS

DEFINITION

AR542471

ACCESSION

AR542471.1

VERSION

GI:53934937

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1464)

Donoho G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B. and Sands, A.T.

Human proteins and polynucleotides encoding the same

JOURNAL

Patent: US 6743907-A 1 01-JUN-2004;

Lexicon Genetics Incorporated; The Woodlands, TX

FEATURES

Location/Qualifiers

source

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linear PAT 08-OCT-2004

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RESULT 2
LOCUS AX118816 1464 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1 from Patent WO0129219.
ACCESSION AX118816
VERSION AX118816.1 GI:14035774
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
TITLE Human cub-domain-containing protein and gene encoding the same
JOURNAL Patent: WO 0129219-A 1 26-APR-2001;
Lexicon Genetics Incorporated (US)
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Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 GGAAGTATGACTGTTTCCAAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT 240
DB 181 GGAAGTATGACTGTTTCCAAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT 240
QY 241 GAGAGTGGATCCCACTTTCTGGCCGGGGTTTTTGTGCTGACTATGCGAGCAGGACCAT 300
DB 241 GAGAGTGGATCCCACTTTCTGGCCGGGGTTTTTGTGCTGACTATGCGAGCAGGACCAT 300
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATATTTTGAAGACAGAAATACAGAAA 360
DB 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATATTTTGAAGACAGAAATACAGAAA 360
QY 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGATATGTTAGATGGA 420
DB 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGATATGTTAGATGGA 420
QY 421 TATAGAGATACCTCTTTATTTGTCGAAAGCTGCCATCCATCAGAGAAATATGCTGATGAA 480
DB 421 TATAGAGATACCTCTTTATTTGTCGAAAGCTGCCATCCATCAGAGAAATATGCTGATGAA 480
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Qy	481	CTAGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCCGATATGAAGGGATTCGTG	540
Db	481	CTAGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCCGATATGAAGGGATTCGTG	540
Qy	541	GCCAAATGCTGTTCTTTTCAGGGATGGTTCCCTGTGTCAGACAAGCCGATTTCTGTTCACCTCC	600
Db	541	GCCAAATGCTGTTCTTTTCAGGGATGGTTCCCTGTGTCAGACAAGCCGATTTCTGTTCACCTCC	600
Qy	601	AATGGTTGCAGCAGATCCTTCAGATTTGAACTGACGGGCAAAATCAGAGCTTCCTTCCTCA	660
Db	601	AATGGTTGCAGCAGATCCTTCAGATTTGAACTGACGGGCAAAATCAGAGCTTCCTTCCTCA	660
Qy	661	TGGCAGTCGGTCAATGACAGTGGAGACCAAGTTCACTGTCTCTCTGGCCAAAGCCCGACTT	720
Db	661	TGGCAGTCGGTCAATGACAGTGGAGACCAAGTTCACTGTCTCTCTGGCCAAAGCCCGACTT	720
Qy	721	CAGGACCAAGGCCAATCATGCGCTTCGGGCGACAGTAGCAACAACCAACACACGAGAG	780
Db	721	CAGGACCAAGGCCAATCATGCGCTTCGGGCGACAGTAGCAACAACCAACACACGAGAG	780
Qy	781	TGGCTTGGAGATCGAATTTGGGGGAGAAAAGAAATACAGAAATTAGGACCAAGGATCT	840
Db	781	TGGCTTGGAGATCGAATTTGGGGGAGAAAAGAAATACAGAAATTAGGACCAAGGATCT	840
Qy	841	ACACAGTCCGAACCTTCAACTTTATGTTAAAGAGTTTGTGTGATGAACCTTCAAAAAACAATAAT	900
Db	841	ACACAGTCCGAACCTTCAACTTTATGTTAAAGAGTTTGTGTGATGAACCTTCAAAAAACAATAAT	900
Qy	901	TCTAAGTGGAGACCTATAAGGAATTTGTAATTAATGAGAAAAGTTGTTTCAGGGTAAC	960
Db	901	TCTAAGTGGAGACCTATAAGGAATTTGTAATTAATGAGAAAAGTTGTTTCAGGGTAAC	960
Qy	961	TCTAACTTTTCGGGACCCAGTGCACAAAACAATTTTCACTCCTCCATCGTGGCCAGATATGTG	1020
Db	961	TCTAACTTTTCGGGACCCAGTGCACAAAACAATTTTCACTCCTCCATCGTGGCCAGATATGTG	1020
Qy	1021	CGGTTGTCCCCAGACATGCGCACAGAGGATAGCCTTGAAGTGGAGCTCATTTGGTTGC	1080
Db	1021	CGGTTGTCCCCAGACATGCGCACAGAGGATAGCCTTGAAGTGGAGCTCATTTGGTTGC	1080
Qy	1081	CAGATTAACAAGGTAAATGATTCAATGCTGTGGCGCAAGACAAGTCAAGCACCAGTGTT	1140
Db	1081	CAGATTAACAAGGTAAATGATTCAATGCTGTGGCGCAAGACAAGTCAAGCACCAGTGTT	1140
Qy	1141	TCAACTAAGAAAGAAGATGAGACAATCAAGGCCCATCCCTTCGGAGAAACATCCACA	1200
Db	1141	TCAACTAAGAAAGAAGATGAGACAATCAAGGCCCATCCCTTCGGAGAAACATCCACA	1200
Qy	1201	GGAAATTAACATTACAACGGTGGCTATTCCATTTGCTGTCTCTTGTGTTCTCGTGGTTGCT	1260
Db	1201	GGAAATTAACATTACAACGGTGGCTATTCCATTTGCTGTCTCTTGTGTTCTCGTGGTTGCT	1260
Qy	1261	GGAAATGGGGATCTTTTGACGCTTTAGAAAAGAAGAAGAAAGGAAGTCCGTATGGATCA	1320
Db	1261	GGAAATGGGGATCTTTTGACGCTTTAGAAAAGAAGAAGAAAGGAAGTCCGTATGGATCA	1320
Qy	1321	CGCGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG	1380
Db	1321	CGCGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG	1380
Qy	1381	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAAGGAGATGACACAAAAAGTTAGATCTC	1440
Db	1381	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAAGGAGATGACACAAAAAGTTAGATCTC	1440
Qy	1441	ATCAACAAGTGATATGGCAGGTTAA	1464
Db	1441	ATCAACAAGTGATATGGCAGGTTAA	1464

RESULT 3
AR542473
LOCUS

DEFINITION	Sequence 5 from patent US 6743907.
ACCESSION	AR542473
VERSION	AR542473.1 GI:53934939
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1620)
TITLE	Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
JOURNAL	Human proteins and polynucleotides encoding the same
Patent:	US 6743907-A 5 01-JUN-2004;
Lexicon Genetics Incorporated; The Woodlands, TX	
FEATURES	Location/Qualifiers
source	1..1620
ORIGIN	/organism="unknown" /mol_type="genomic DNA"
Query Match	100.0%; Score 1464; DB 6; Length 1620;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1464; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACACTGTTTGCAGAAAGACAAATT 60
Db	157 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACACTGTTTGCAGAAAGACAAATT 216
Qy	61 ACAGTACCAAGGGGAAAGACATGATCTGAGGTTGGGAGATTGGATATCGAATCCCAG 120
Db	217 ACAGTACCAAGGGGAAAGACATGATCTGAGGTTGGGAGATTGGATATCGAATCCCAG 276
Qy	121 ACCTGTGCTTCTGACTATCTTCTCTTACCAGGCTCTTCAGATCAATATGTCCTCACTACTGT 180
Db	277 ACCTGTGCTTCTGACTATCTTCTCTTACCAGGCTCTTCAGATCAATATGTCCTCACTACTGT 336
Qy	181 GGAAGTATGACTGTGTCCCAAGAACTCTTGTTGAAACAAGTGAAGTAACCGTCCGCTTT 240
Db	337 GGAAGTATGACTGTGTCCCAAGAACTCTTGTTGAAACAAGTGAAGTAACCGTCCGCTTT 396
Qy	241 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGCTGACCTATCGGAGCAGCGACCAT 300
Db	397 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGCTGACCTATCGGAGCAGCGACCAT 456
Qy	301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAATAACAGCAA 360
Db	457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAATAACAGCAA 516
Qy	361 TTCTGCCACGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
Db	517 TTCTGCCACGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 576
Qy	421 TATAGATACCTCTTTATTTGTCAAAGCTGCCATCCATGTCAGGAATAATTGCTGATGAA 480
Db	577 TATAGATACCTCTTTATTTGTCAAAGCTGCCATCCATGTCAGGAATAATTGCTGATGAA 636
Qy	481 CTAGGTGGCCAGATCATGATGTCCTTACGCGCAAAGGATCAGTCGATGAAAGGATTCGTG 540
Db	637 CTAGGTGGCCAGATCATGATGTCCTTACGCGCAAAGGATCAGTCGATGAAAGGATTCGTG 696
Qy	541 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGCGATTTCTGTTTACCTCC 600
Db	697 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGCGATTTCTGTTTACCTCC 756
Qy	601 AATGGTTGACAGAGATCCTTTGAGTTTTGAACTGTACGGGCAATCAGAGCTTCTTCTCA 660
Db	757 AATGGTTGACAGAGATCCTTTGAGTTTTGAACTGTACGGGCAATCAGAGCTTCTTCTCA 816
Qy	661 TGGCAGTCCGTCATGAGAGTGGAGACCAAGTTCACTGTCCTCTGCGCAAGCCGACTT 720
Db	817 TGGCAGTCCGTCATGAGAGTGGAGACCAAGTTCACTGTCCTCTGCGCAAGCCGACTT 876
Qy	721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAAACCAACAAACACAGAG 780

Db 877 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACAAACCAAAACACAGAG 936
Qy 781 TGGCTGAGATCGATTGGGGGAGAAAGAAATAAAGAGAAATTAAGGACCAACAGATCT 840
Db 937 TGGCTGAGATCGATTGGGGGAGAAAGAAATAAAGAGAAATTAAGGACCAACAGATCT 996
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 997 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTGTGATGAACCTTCAAAAACAATAAT 1056
Qy 901 TCTAAGTGAAGACCTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGCTAAC 960
Db 1057 TCTAAGTGAAGACCTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGCTAAC 1116
Qy 961 TCTAAGTTCGGGACCCAGTGCACAAACATTTTCATCCCTCCCATCTGGCCAGATATGTG 1020
Db 1117 TCTAAGTTCGGGACCCAGTGCACAAACATTTTCATCCCTCCCATCTGGCCAGATATGTG 1176
Qy 1021 CGGGTTGTCCCCAGACATGCGACAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1177 CGGGTTGTCCCCAGACATGCGACAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1236
Qy 1081 CAGATTACAAAGTAAATGATTCATTGGTGTGGCGCAAGCAAGTCAAAAGCCAGTGTT 1140
Db 1237 CAGATTACAAAGTAAATGATTCATTGGTGTGGCGCAAGCAAGTCAAAAGCCAGTGTT 1296
Qy 1141 TCAACTAAGAAAGAGATGAGCAATCACAAAGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1297 TCAACTAAGAAAGAGATGAGCAATCACAAAGCCCATCCCTCGGAAGAAACATCCACA 1356
Qy 1201 GGAATAAACATTACAAAGGTGGCTATTCATTTGGTGTCTCTTGTGTCTGGTGTGTTGCT 1260
Db 1357 GGAATAAACATTACAAAGGTGGCTATTCATTTGGTGTCTCTTGTGTCTGGTGTGTTGCT 1416
Qy 1261 GGAATGGGATCTTTCAGGCTTTAGAAAGAGAGAGAAAGAGTCCGTATGATCA 1320
Db 1417 GGAATGGGATCTTTCAGGCTTTAGAAAGAGAGAGAAAGAGTCCGTATGATCA 1476
Qy 1321 GCGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATATCCCTTTCAGACATCAG 1380
Db 1477 GCGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATATCCCTTTCAGACATCAG 1536
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGAGAGATGACACAAAAGTTAGATCTC 1440
Db 1537 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGAGAGATGACACAAAAGTTAGATCTC 1596
Qy 1441 ATCAAGTGTATGGCAGGTTAA 1464
Db 1597 ATCAAGTGTATGGCAGGTTAA 1620

RESULT 4
AX118820
LOCUS AX118820 1620 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 5 from Patent WO0129219.
ACCESSION AX118820
VERSION AX118820.1 GI:14035776
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human cub-domain-containing protein and gene encoding the same
JOURNAL Patent: WO 0129219-A 5 26-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source 1..1620
/organism="Homo sapiens"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1464; DB 6; Length 1620;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/db_xref="taxon:9606"
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Db 157 ATGACATCTAAGAAATATATCCCGGACCTTACCCTTACACACTGTTTGGGAAAAGACAAT 216
Qy 61 ACAGTACCAAAAGGGGAAAAGACTGATCTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 120
Db 217 ACAGTACCAAAAGGGGAAAAGACTGATCTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 276
Qy 121 ACTGTGCTCTTGACTATATCTTCTTCCACGAGCTTTCAGATCAATATGTCATCTACTGT 180
Db 277 ACTGTGCTCTTGACTATATCTTCTTCCACGAGCTTTCAGATCAATATGTCATCTACTGT 336
Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTTCTTGTGGAACACAAAGTGAAGTAAACCGTCCGCTTT 240
Db 337 GGAAGTATGACTGTTCCCAAGAACTCTTCTTGTGGAACACAAAGTGAAGTAAACCGTCCGCTTT 396
Qy 241 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTCTGCTGACCTATTCGAGCAGCGACCAT 300
Db 397 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTCTGCTGACCTATTCGAGCAGCGACCAT 456
Qy 301 CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTATTTTGAAGACAGAAATACAGAAA 360
Db 457 CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTATTTTGAAGACAGAAATACAGAAA 516
Qy 361 TTCGCCCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
Db 517 TTCGCCCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 576
Qy 421 TATAGAGTATACCTCTTTATTTGTGAAAGCTGCCATCCATGCGAGCAATATTTGCTGATGA 480
Db 577 TATAGAGTATACCTCTTTATTTGTGAAAGCTGCCATCCATGCGAGAAATATTTGCTGATGA 636
Qy 481 CTAGTGGGCGCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTGCATATGAAGGGATTTCTG 540
Db 637 CTAGTGGGCGCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTGCATATGAAGGGATTTCTG 696
Qy 541 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTACAGCAAGCGATTTCTGTTTACCTCC 600
Db 697 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTACAGCAAGCGATTTCTGTTTACCTCC 756
Qy 601 AATGGTTGCGAGCAGATCCTTGGATTTTGAACCTTGACGGGCAATTCAGAGCTTCTTCTCTCA 660
Db 757 AATGGTTGCGAGCAGATCCTTGGATTTTGAACCTTGACGGGCAATTCAGAGCTTCTTCTCTCA 816
Qy 661 TGGCAGTCCGCTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTCTGCCAAGCCGACTT 720
Db 817 TGGCAGTCCGCTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTCTGCCAAGCCGACTT 876
Qy 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACACCAACCAACCGAGAG 780
Db 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACACCAACCAACCGAGAG 936
Qy 781 TGGCTGAGATCGATTGGGGGAGAAAGAAATAAAGAGAAATTAAGGATTCAGGGTAACT 840
Db 937 TGGCTGAGATCGATTGGGGGAGAAAGAAATAAAGAGAAATTAAGGATTCAGGGATTC 996
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 997 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTGTGATGAACCTTCAAAAACAATAAT 1056
Qy 901 TCTAAGTGAAGACCTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGCTAAC 960
Db 1057 TCTAAGTGAAGACCTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGCTAAC 1116
Qy 961 TCTAAGTTCGGGACCCAGTGCACAAACATTTTCATCCCTCCCATCTGGCCAGATATGTG 1020

Db	1117	TCCTAACTTTCCGGACCCAGTGCAGAAACAAATTTTCATCCCTCCCATCGTGGCCAGATATGTG	1176	QY	181	GGAGATATGACTGTTCCCAAGAACTCTTGTGTAACCAAGTGAAGTAAACCGTCCGCTTT	240
QY	1021	CGGTTGTGTCCTCCAGACATGCGACAGAGGATACCTTTGAAGTGGAGCTCATTTGGTTGC	1080	Db	478	GGAGATATGACTGTTCCCAAGAACTCTTGTGTAACCAAGTGAAGTAAACCGTCCGCTTT	537
Db	1177	CGGTTGTGTCCTCCAGACATGCGACAGAGGATACCTTTGAAGTGGAGCTCATTTGGTTGC	1236	QY	241	GAGAGTGGATCCACATTTCTGCCCAGGTTTCTGCTGACCTATATGCGAGCAGCGACAT	300
QY	1081	CAGATTACACAAGGTAATGATTTCATTTGGTGTGGCGCAAGCAAAAGTCAAAGCACCAGTGT	1140	Db	538	GAGAGTGGATCCACATTTCTGCCCAGGTTTCTGCTGACCTATATGCGAGCAGCGACAT	597
Db	1237	CAGATTACACAAGGTAATGATTTCATTTGGTGTGGCGCAAGCAAAAGTCAAAGCACCAGTGT	1296	QY	301	CCAGATTTTAATACATGTTTGGAAACGAGCTAGCCATATTTGAAGACAGATACAGCAAA	360
QY	1141	TCAACTAAGAAAGAGATGAGCAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA	1200	Db	598	CCAGATTTTAATACATGTTTGGAAACGAGCTAGCCATATTTGAAGACAGATACAGCAAA	657
Db	1297	TCAACTAAGAAAGAGATGAGCAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA	1356	QY	361	TTCTGCCCAGCTGGTTGTAGAGACGTTAGCAGAGAGACATTTCTGGGAATATGGTAGATGA	420
QY	1201	GGAAATAACAATTACCAAGTGGCTATTCCATTTGGTGTGGCGCAAGCAAAAGTCAAAGCACCAGTGT	1260	Db	658	TTCTGCCCAGCTGGTTGTAGAGACGTTAGCAGAGAGACATTTCTGGGAATATGGTAGATGA	717
Db	1357	GGAAATAACAATTACCAAGTGGCTATTCCATTTGGTGTGGCGCAAGCAAAAGTCAAAGCACCAGTGT	1416	QY	421	TATAGAGATACTCTTTTATTTGTGCAAAAGCTGCCATCCATGCGAGGAATAATTTGCTGATGAA	480
QY	1261	GGAAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGTCCGTTATGGATCA	1320	Db	718	TATAGAGATACTCTTTTATTTGTGCAAAAGCTGCCATCCATGCGAGGAATAATTTGCTGATGAA	777
Db	1417	GGAAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGTCCGTTATGGATCA	1476	QY	481	CTAGGTGGCCAGATCAGTGTCTTCCAGCGCAAAAGGATCAGTGCATATGAGGGATTTCTG	540
QY	1321	GCGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCGCAGATCAG	1380	Db	778	CTAGGTGGCCAGATCAGTGTCTTCCAGCGCAAAAGGATCAGTGCATATGAGGGATTTCTG	837
Db	1477	GCGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCGCAGATCAG	1536	QY	541	GCCAAATGGTGTCTTTTCGAGGGATGTTCCCTGTGAGACAAAGCGATTTCTGTTTACCTCC	600
QY	1381	TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACAAAGTTAGATCTC	1440	Db	838	GCCAAATGGTGTCTTTTCGAGGGATGTTCCCTGTGAGACAAAGCGATTTCTGTTTACCTCC	897
Db	1537	TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACAAAGTTAGATCTC	1596	QY	601	AATGGTTGAGCAGATCTTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCTCA	660
QY	1441	ATCACAAGTGATATGCGAGTTAA	1464	Db	898	AATGGTTGAGCAGATCTTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCTCA	957
Db	1597	ATCACAAGTGATATGCGAGTTAA	1620	QY	661	TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACCTGCTCTCTGCGCAAGCCGACTT	720
RESULT 5				Db	958	TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACCTGCTCTCTGCGCAAGCCGACTT	1017
AR542472				QY	721	CAGGACCAAGGCCCATCATGCGCTTCGCGGACAGTAGCAACCAACCAACCAACCAAGAG	780
LOCUS	AR542472	1761 bp	DNA	Db	1018	CAGGACCAAGGCCCATCATGCGCTTCGCGGACAGTAGCAACCAACCAACCAACCAAGAG	1077
DEFINITION	Sequence 3 from patent US 6743907.		linear	QY	781	TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAATAACAGGAATTAGGACCAAGGATCT	840
ACCESSION	AR542472			Db	1078	TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAATAACAGGAATTAGGACCAAGGATCT	1137
VERSION	AR542472.1	GI:53934938		QY	841	ACACAGTGGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTCAAAACATATAT	900
KEYWORDS	Unknown.			Db	1138	ACACAGTGGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTCAAAACATATAT	1197
SOURCE	Unknown.			QY	901	TCTAAGTGGAACTTCAACTTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC	960
ORGANISM	Unclassified.			Db	1198	TCTAAGTGGAACTTCAACTTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC	1257
REFERENCE	1 (bases 1 to 1761)			QY	961	TCTAAGTGGAACTTCAACTTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC	1020
AUTHORS	Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.			Db	1258	TCTAAGTGGAACTTCAACTTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC	1317
TITLE	Human proteins and polynucleotides encoding the same			QY	1021	CGGGTGTGCCCCCAGACATGGCCACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC	1080
JOURNAL	Patent: US 6743907-A 3 01-JUN-2004;			Db	1318	CGGGTGTGCCCCCAGACATGGCCACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC	1377
FEATURES	Lexicon Genetics Incorporated; The Woodlands, TX			QY	1081	CAGATTACACAAGGTAATGATTTCATTTGGTGTGGCGCAAGCAAAAGTCAAAGCACCAGTGT	1140
source	Location/Qualifiers			Db	1378	CAGATTACACAAGGTAATGATTTCATTTGGTGTGGCGCAAGCAAAAGTCAAAGCACCAGTGT	1437
ORIGIN	1. :1761			QY	1141	TCAACTAAGAAAGAGATGAGCAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA	1200
Query Match	100.0%; Score 1464; DB 6; Length 1761;			Db	1438	TCAACTAAGAAAGAGATGAGCAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA	1497
Best Local Similarity	100.0%; Pred. No. 0;			QY	1201	GGAAATAACAATTACCAAGTGGCTATTCCATTTGGTGTGGCGCAAGCAAAAGTCAAAGCACCAGTGT	1260
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Db	1498	GGAAATAACAATTACCAAGTGGCTATTCCATTTGGTGTGGCTCTTGTGCTCTGTTGCT	1557
QY	1	ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGCGAAAGACAATT	60	QY	1261	GGAAATGGGATCTTTTGCAGCCCTTTAGAAAGAAAGAAAGGAAAGTCCGTTATGGATCA	1320
Db	298	ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGCGAAAGACAATT	357				
QY	61	ACAGTACCAAGGGGAAAGACATGATTTCTGAGTTGGGAGATTTGGATATCGAATCCCAAG	120				
Db	358	ACAGTACCAAGGGGAAAGACATGATTTCTGAGTTGGGAGATTTGGATATCGAATCCCAAG	417				
QY	121	ACCTGTGCTTCTGACTATCTTCTTCCAGGCTCTTCAGATCAATATGGTCCACTGTT	180				
Db	418	ACCTGTGCTTCTGACTATCTTCTTCCAGGCTCTTCAGATCAATATGGTCCACTGTT	477				

Db 1558 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAGTCCGTATGATCA 1617
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Db 1618 GGGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATCCCTTCCGACATCAG 1677
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Db 1738 ATCAAGTATGATGGAGTTAA 1761
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RESULT 6
AX118818 1761 bp DNA linear PAT 11-MAY-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0129219.
ACCESSION AX118818
VERSION AX118818.1 GI:14035775

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.

TITLE Human cub-domain-containing protein and gene encoding the same
JOURNAL Patent: WO 0129219-A 3 26-APR-2001;
Lexicon Genetics Incorporated (US)

FEATURES
source
1..1761
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 100.0%; Score 1464; DB 6; Length 1761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAATT 60
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Db 298 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAATT 357
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Qy 61 ACAGTACCAAGGGGAAAGAGTCTGATCTGAGGTTGGGAGATTTGGATATCGAATCCAG 120
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Db 358 ACAGTACCAAGGGGAAAGAGTCTGATCTGAGGTTGGGAGATTTGGATATCGAATCCAG 417
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Qy 121 ACCTGTGCTCTGACTATCTCTTCAACAGCTCTTCAGATCAATATGGTCCATCTGT 180
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Db 418 ACCTGTGCTCTGACTATCTCTTCAACAGCTCTTCAGATCAATATGGTCCATCTGT 477
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Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTGTTTGAACACAGTGAAGTAACCGTCGCTTT 240
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Qy 481 CTAGGTGGCCAGATCAGTGTGCTTCAGGCGAAAGGATCAGTCGATATCAAGGGATTCG 540
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Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATTAACAGGAATTAGGACCAAGGATCT 840
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Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGTGATGAATTTCAAAAAACAATA 900
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Qy 961 TCTAAGTGGAGACCTATATAAGGAATTTGTAATTAATGAAGAAAGGTTTTCAGGGTAAC 1020
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RESULT 7

AR542474
LOCUS 1768 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 7 from patent US 6743907.
AR542474
ACCESSION AR542474.1 GI:53934940
VERSION AR542474.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: US 6743907-A 7 01-JUN-2004;
Lexicon Genetics Incorporated; The Woodlands, TX
FEATURES
source 1.1768
/organism="unknown"
/mol_type="genomic DNA"

Query Match 100.0%; Score 1464; DB 6; Length 1768;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGGGAAGAGCAATT 60
DB |||||||
QY 59 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGGGAAGAGCAATT 118
DB |||||||
QY 61 ACAGTACCAAAGGGGAAAGACTGATTCGAGGTGGGAGATTGGATATCGAATCCCAG 120
DB |||||||
QY 119 ACAGTACCAAAGGGGAAAGACTGATTCGAGGTGGGAGATTGGATATCGAATCCCAG 178
DB |||||||
QY 121 ACCGTGCTCTCACTATCTCTTCCACAGCTCTTCAGATCAATATGTCATCTGT 180
DB |||||||
QY 179 ACCGTGCTCTCACTATCTCTTCCACAGCTCTTCAGATCAATATGTCATCTGT 238
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QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTCAACACAGTCAAGTAAACCGTCCGCTTT 240
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QY 239 GGAAGTATGACTGTTCCCAAGAACTCTTGTCAACACAGTCAAGTAAACCGTCCGCTTT 298
DB |||||||
QY 241 GAGAGTGGATCCACATTTCTGGCGGGTTTTTGTGACCTATTCGAGCAGCGACCAT 300
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QY 301 CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTTGAAGACAGAAATACAGAAA 360
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DB |||||||
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DB |||||||
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DB |||||||
QY 541 GCCAATGGTGTCTTTCTGGAGGATGTTCTCTGACAGACAGGATTTCTGTTTACCTCC 600
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DB |||||||
QY 899 ACACAGTCGAACCTTCAACTTTTATGTTAAGATTTTGTGATGAACCTTCAAAAACAATAAT 958
DB |||||||
QY 901 TCTAAGTGGAGAGACCTTATAAGCAATTGTGAATAATGAAGAAAGGTTTTCAGGGTAAC 960
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QY 1499 ATCACAAGTGTATGTCAGGTTAA 1522
DB |||||||

RESULT 8

AX118822
LOCUS 1768 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 7 from Patent WO0129219.
AX118822
ACCESSION AX118822
VERSION AX118822.1 GI:14035777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
AUTHORS Sands, A.T.
TITLE Human cub-domain-containing protein and gene encoding the same
JOURNAL Patent: WO 0129219-A 7 26-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES Location/Qualifiers

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source 1. .1768
/organism="Homo sapiens"
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ORIGIN

Query Match 100.0%; Score 1464; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACAACCTGTTTGGGAAAGACAATT 60
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DB 419 TTCTGCCAGCTGGTGTAGAGAGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 478
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RESULT 9
CQ870614
LOCUS CQ870614
DEFINITION Sequence 23 from Patent WO2004073657.
ACCESSION CQ870614
VERSION CQ870614.1 GI:52000125
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Aziz,N., Gish,K.C., Wilson,K.E. and Zlotnik,A.
TITLE Methods of diagnosis of cancer, composition and methods of
screening for modulators of cancer
JOURNAL Patent: WO 2004073657-A 23 02-SEP-2004;
PROTEIN DESIGN LABS, INC. (US)
FEATURES
source 1. .2010
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ORIGIN

Query Match 99.9%; Score 1462.4; DB 6; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACAACCTGTTTGGGAAAGACAATT 60
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Db 582 CCAGATTTAATAACATGTTTGGACAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 641
Qy 361 TTCTGCCAGCTGGTTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGA 420
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RESULT 10
LOCUS CQ870615 2010 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 24 from Patent WO2004073657.
ACCESSION CQ870615
VERSION CQ870615.1 GI:52000126
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Aziz,N., Gish,K.C., Wilson,K.E. and Zlotnik,A.
TITLE Methods of diagnosis of cancer, composition and methods of
screening for modulators of cancer
JOURNAL Patent: WO 2004073657-A 24 02-SEP-2004;
PROTEIN DESIGN LABS, INC. (US)
FEATURES
SOURCE 1. .2010
Location/Qualifiers
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ORIGIN
Query Match 99.9%; Score 1462.4; DB 6; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
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BC035671

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(cDNA clone MGC:46341 IMAGE:5730536), complete cds.

ACCESSION BC035671
VERSION BC035671.1 GI:23274238

KEYWORDS MGC.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 2010)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Loquellano, N.A., Peters, G.J.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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CONSRM
TITLE

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL
PUBMED

12477932
2 (bases 1 to 2010)

AUTHORS
CONSRM

NIH MGC Project
Direct Submission

TITLE
JOURNAL

Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK
COMMENT

Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayèle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAC Plate: 79 Row: i Column: 21
This clone was selected for full length sequencing because it

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ORIGIN

Query Match 99.9%; Score 1462.4; DB 8; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTGGCGAAAGACAATT 60
DB 282 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTGGCGAAAGACAATT 341
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Sequence 47 from Patent WO0202634.
DEFINITION
AX704743
ACCESSION
AX704743.1
VERSION
GI:29561409
KEYWORDS
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PAT 04-APR-2003


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          Hominoidea; Homo.

REFERENCE
AUTHORS Gururajan, R., Hafalia, A.J., Kallick, D.A., Patterson, C., Azimzai, Y.,
        Khan, F.A., Xu, Y., Yao, M.G., Yue, H., Au-Young, J., Batra, S.,
        Baughn, M.R., Borowsky, E.A., Lu, T.P., Lu, D.A., Lu, Y., Tang, Y.T.,
        Yang, J., Zingler, K.A., Deleage, A.M., Gietzen, K., Marcus, G.A.,
        Nguyen, D.B., Policky, J.L., Ramkumar, J., Thangavelu, K., Wallia, N.K.
        and Warren, B.A.
TITLE Human extracellular matrix and cell adhesion polypeptides
JOURNAL Patent: WO 0202634-A 47 10-JAN-2002;
INCYTE GENOMICS INC. (US)
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Best Local Similarity 99.94; Pred. No. 0;
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VERSION CO413296.1 GI:41321077
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REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
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        Patent: WO 0170979-A 20367 27-SEP-2001;
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACA CTGTTGCGGAAAAGACAATT 60
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QY 481 CTAGTGGCCAGATCAGTGTGCTTTCAGCGAAAGGATCAGTGCATATGAAGGATCTTG 540
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VERSION AX833875.1 GI:39920010
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Isoigai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and
Masuho, Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 999 24-SEP-2003;
RESEARCH Association for Biotechnology (JP)
FEATURES Location/Qualifiers
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QY	721	CAGGACCAAGGCCCATCATGGCTTCGGCGACAGTAGCAACCAACCAACCAACGAGAG	780	AUTHORS	Oca,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamanoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahara,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hirakawa,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Sashihara,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Otsuki,T., Kobatake,N., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kawakami,T., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigetani,K., Senba,T., Matsuura,K., Nagajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.	984	TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs			
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AUTHORS

Nishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished

TITLE

JOURNAL

REFERENCE

3 (bases 1 to 2547)

AUTHORS

Isogai, T. and Yamamoto, J.

TITLE

Direct Submission

JOURNAL

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5' - & 3' - end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

FEATURES

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Location/Qualifiers

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Best Local Similarity 99.5%; Pred. No. 0;
Matches 1456; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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2	2557	100.0	1620	3	US-09-691-344A-5
3	2557	100.0	1761	3	US-09-691-344A-3
4	2557	100.0	1768	3	US-09-691-344A-7
5	1146.5	44.8	1871	3	US-09-823-038A-43
6	867.5	33.9	2310	3	US-10-191-436A-7
7	867.5	33.9	2310	3	US-10-191-436A-9
8	860.5	33.7	2328	3	US-10-191-436A-1
9	860.5	33.7	2328	3	US-10-191-436A-3

10	856.5	33.5	2310	3	US-10-191-436A-4	Sequence 4, Appli
11	856.5	33.5	2310	3	US-10-191-436A-6	Sequence 6, Appli
12	331.5	13.0	3371	3	US-09-116-473-1	Sequence 1, Appli
13	329.5	12.9	2730	3	US-08-936-135-17	Sequence 17, Appli
14	329.5	12.9	2730	3	US-09-439-711C-17	Sequence 17, Appli
15	329.5	12.9	2781	3	US-08-936-135-19	Sequence 19, Appli
16	329.5	12.9	2781	3	US-09-439-711C-19	Sequence 19, Appli
17	329.5	12.9	3404	3	US-09-583-638-3	Sequence 3, Appli
18	324.5	12.7	3539	3	US-08-936-135-7	Sequence 7, Appli
19	324.5	12.7	3539	3	US-09-439-711C-7	Sequence 7, Appli
20	324.5	12.7	4718	3	US-08-936-135-9	Sequence 9, Appli
21	324.5	12.7	4718	3	US-09-439-711C-9	Sequence 9, Appli
22	324.5	12.7	4733	3	US-08-936-135-11	Sequence 11, Appli
23	324.5	12.7	4733	3	US-09-439-711C-11	Sequence 11, Appli
24	324.5	12.7	4765	3	US-08-936-135-21	Sequence 21, Appli
25	324.5	12.7	4765	3	US-09-439-711C-21	Sequence 21, Appli
26	324.5	12.7	4769	3	US-08-936-135-13	Sequence 13, Appli
27	324.5	12.7	4769	3	US-09-439-711C-13	Sequence 13, Appli
28	324.5	12.7	4780	3	US-08-936-135-23	Sequence 23, Appli
29	324.5	12.7	4780	3	US-09-439-711C-23	Sequence 23, Appli
30	324.5	12.7	4784	3	US-08-936-135-15	Sequence 15, Appli
31	324.5	12.7	4784	3	US-09-439-711C-15	Sequence 15, Appli
32	321	12.6	6893	3	US-09-054-272-37	Sequence 37, Appli
33	321	12.6	6914	3	US-09-949-002-6	Sequence 6, Appli
34	321	12.6	6987	3	US-09-949-002-231	Sequence 231, App
35	318	12.4	6585	3	US-08-746-111-4	Sequence 4, Appli
36	317	12.4	6585	2	US-08-804-196-1	Sequence 1, Appli
37	317	12.4	6909	2	US-08-658-340-1	Sequence 1, Appli
38	317	12.4	6909	3	US-08-746-111-26	Sequence 26, Appli
39	317	12.4	6909	3	US-08-454-353A-1	Sequence 1, Appli
40	317	12.4	6909	3	US-09-165-019-1	Sequence 1, Appli
41	308	12.0	7032	3	US-09-324-867-1	Sequence 1, Appli
42	303	11.8	2772	3	US-08-936-135-1	Sequence 1, Appli
43	303	11.8	2772	3	US-09-439-711C-1	Sequence 1, Appli
44	301.5	11.8	1384	2	US-07-607-538C-1	Sequence 1, Appli
45	301.5	11.8	1384	2	US-08-162-402B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-691-344A-1
; Sequence 1, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-1

Alignment Scores:
Pred. No.: 1.35e-279 Length: 1464
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0


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QY 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 217 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 276
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 277 ACCTGTGCTCTCGACTATCTCTCTCCACAGCTCTTCAGATCAATATGGTCCATACGT 336
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 337 GGAAGTATGACTGTTCCTCCAAAGAACTCTTGTGAAACACAGTGAAGTAAACCGTCGCTTT 396
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 397 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTGACCTATCGGAGCAGCGACCAT 456
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 457 CCAGATTTTAAACATGTTTGGAAACGAGCTAGCCATTATTGAAGACAGAAATACAGCAA 516
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 517 TTCTGCCAGCTGGTGTAGACCGTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 576
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleAlaAspGlu 160
DB 577 TATAGAGATACCTCTTATTGTGCAAGCTGCCATCCATCGAGGAATATTCTGATGAA 636
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 697 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGCATTTCTGTTTACCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 757 AATGTTGCGAGATCCTTGTAGTTTGTAACTGACGGCAATCAGAGCTTCTCTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACGTGCTCTCTGGCCAGCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGGCTTGGGGCGACAGTAGCAACCAACCAACCAAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGlySer 280
DB 937 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATAACAGGAATTAGGCCACAGATCT 996
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPhelysAsnAsn 300
DB 997 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTGTGATGAACCTTCAAAACAATAAT 1056
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGGAGACCTTATAAGGAATTTGGAATAATGAAGAAAGGTGTTTCAGGGTAAAC 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1117 TCTAATCTTGGGACCCAGTGGCAAAACAATTTTCATCTCCCTCCCATGTGGCCAGATATGTG 1176
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValLeuIleGlyCys 360
DB 1177 CGGGTGTGCCCCAGACATGGCACCAGAGATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1236
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTACAAAGGTAATGATTCATTTGGTGTGGCGCAAGACAAAGTCAAAGCCAGTGT 1296
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QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCACCTAAGAAAGAGATGAGCAATCAGAGCCCATCCCTCGGAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
DB 1357 GGAATAAACAATTAACAACGGTGGCTATTCCATTGGTGCTCTTGTGCTCTGGTGTGCT 1416
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
DB 1417 GGAATGGGGATCTTTGACGCCCTTTAGAAAGAAAGAAAGAAAGAGTCCGTATGGATCA 1476
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1477 GCGGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1537 TCAGCTGAGTTTACCATTACCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC 1596
QY 481 IleThrSerAspMetAlaGly 487
DB 1597 ATCAAGTGATATGGCAGGT 1617

RESULT 3
US-09-691-344A-3
; Sequence 3, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-3

Alignment Scores:
Pred. NO.: 1,85e-279 Length: 1761
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-813-588-2 (1-487) x US-09-691-344A-3 (1-1761)
QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 298 ATGACATCTTAAGAAATTATCCCGGACCTTACCCTTACACACTGTTTGGGAAAGACAAT 357
QY 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 417
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 418 ACCTGTGCTCTCGACTATCTCTCTTCCAGCTCTTTCAGATCAATATGGTCCATACGT 477
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QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 359 CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGATACAGCAA 418
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 419 TTCGTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 478
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 479 TATAGAGATACCTTCTTATTTGTGCAAGCTGCCATCCATGCAGAAATAATTTGTGTAGAA 538
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 539 CTAGGTGGCCAGATCATGTGCTTCAGCGCAAGGGATCATGTCATGAAGGATTCG 598
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 599 GCCAATGGTGTCTTTTCAGGGATGGTTCCCTGCAGACAAGCGATTTCTGTTTACCTCC 658
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 659 AATGGTTCAGCAGATCCCTTGAAGTTTGAACCTGCAGCGGCAAAATCAGAGCTTCTCTCA 718
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 719 TGGCAGTCGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTCGCCAGCCCACTT 778
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 779 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACAACCAACCAACCCAGAG 838
QY 261 TrpLeuGluIleAspLeuGlyLysLysLysLysIleThrGlyIleArgThrGlySer 280
DB 839 TGGCTGGAGATCGATTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGATCT 898
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 899 ACACAGTCGACTTCACTTTTATGTTAGAGTTTGTGATGACTTCAAAACAATAAT 958
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 959 TCTAAGTGAAGACCTATAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAAGGTAAC 1018
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1019 TCTAACTTTTCGGGACCCAGTGCACAAACAATTTTCACTCCCTCCCATCGTGGCCAGATATGT 1078
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1079 CGGGTTGTCCCCAGACATGGCCAGAGATAGCCCTGAAGTGGAGCTCATTTGGTTGC 1138
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1139 CAGATTACACAAGGTAATGATTCACTTGGTGTGGCGCAAGCAAGTCAAGACCAAGTGT 1198
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1199 TCAACTTAAGAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1258
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValValPheAla 420
DB 1259 GGNATHAACATTTACACGGTGGCTATTCATTTGGTCTCTTGTGTCCTGGTGTGTGT 1318
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
DB 1319 GGAATGGGATCTTTTCAGCCTTTAGAAAGAGAGAGAGAGAGAGTCCGTATGGATCA 1378
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1379 GGGAGGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTTCCAGACATCAG 1438

QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1439 TCAGCTGAGTTTACCATCAGCTATGATATATGAGAGGAGATGACACAAAAGTTAGATCTC 1498
QY 481 IleThrSerAspMetAlaGly 487
DB 1499 ATCACAAAGTATATGGCAGGT 1519
RESULT 5
US-09-823-038A-43
; Sequence 43, Application US/09823038A
; Patent No. 6797271
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compositions Isolated From Stromal Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1037c3
; CURRENT APPLICATION NUMBER: US/09/823, 038A
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Mouse
US-09-823-038A-43
Alignment Scores:
Pred. No.: 1,96e-119 Length: 1871
Score: 1146.50 Matches: 236
Percent Similarity: 53.50% Conservative: 24
Best Local Similarity: 48.56% Mismatches: 27
Query Match: 44.84% Indels: 199
DB: 3 Gaps: 1
US-10-813-588-2 (1-487) x US-09-823-038A-43 (1-1871)
QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 193 ATGACATCTAAGATTAATCCAGGACTTACCCCAATACACITGTGTGAAAGATCATC 252
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 253 ACAGTCCCAAGGGGAAGAGACTTATCTGAGGTTGGGAGATTGAACATTCAGTCCAAG 312
QY 41 ThrCysAlaSerAspTyrIleLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 313 ACCTGGCTTCTGACTATCTCTTCAGCAGTGCACAGATCAGTATGGTCCATATGTT 372
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 373 GGGAGTGGGTGTTCCCAAGAACTCCGGCTGAATCAACGAAGTGAATGCTCTCTTC 432
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
DB 433 AAGATGGATCTCACATTTCTGGCGGGGCTTCTGCTGACCTACCCAGCAGTGCACAT 492
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 493 CCAGATTTAATAACCTGTTTGGAAAGCAGGAGCCCATTTATTCGAGGAGAAATACAGCAA 552
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 553 TTCCTCCCAAGCTGGCTGTAGACATAGCAGAGATATTTCTGGGGAATACAAAAGATGT 612
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 613 TACAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCAGCGGAGTATCATCAGATGAA 672

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QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 673 CTAGGTGGCCACATCACTTCTCAGAGCAAGGATAAGTCACTATGAGGACTCCGTG 732
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 733 GCCAATGGCGTGTCTCCCGGCATGTTCTTTCGGAAGAGGATTCCTTTT 786
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
Db 786 ----- 786
QY 221 TrpGlnSerValAsnGlnSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 786 ----- 786
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 786 ----- 786
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
Db 786 ----- 786
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPhelLysAsnAsn 300
Db 786 ----- 786
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
Db 786 ----- 786
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheValAlaArgTyrVal 340
Db 786 ----- 786
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 786 ----- 786
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 786 ----- 786
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluThrThrSerThr 400
Db 787 -----ACACCCCA 795
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
Db 796 GGAATGAATATTACACTGTGGCGATTCCCATCAGTGATTCATCGCCCTCTCTGACT 855
QY 421 GlyMetGlyIlePheAlaAlaPheAtqLysLysLysLysGlySerProTyrGlySer 440
Db 856 GGAATGGGATCTTGGCAATCTGTAGAAAGGAAAAGAAAGAAATCCATATGTGTCA 915
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 916 GCTGACGCTCAGAAAACAGCGCTGTGGAGCAGATTAATATCCCTTTGCCAGGCATCAG 975
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 976 TCGACGGAAATTTACCATCAGTATGACAATGAAAAAGAGATGACACAAAAAGTTGGATCTC 1035
QY 481 IleThrSerAspMetAla 486
Db 1036 ATCACTAGTGATATGGCA 1053
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RESULT 6

US-10-191-436A-7

; Sequence 7, Application US/10191436A

; Patent No. 6900031

GENERAL INFORMATION:

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; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; FILE REFERENCE: 070993
; CURRENT APPLICATION NUMBER: US/10191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2310
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; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(198)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (199)..(2310)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2310)
; US-10-191-436A-7
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Alignment Scores:

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Pred. No.: 1.24e-87 Length: 2310
Score: 867.50 Matches: 207
Percent Similarity: 54.63% Conservative: 94
Best Local Similarity: 37.57% Mismatches: 171
Query Match: 33.93% Indels: 79
DB: 3 Gaps: 17
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US-10-813-588-2 (1-487) x US-10-191-436A-7 (1-2310)

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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 241 CTTCATCATCACTCACTACCCATCACTATCTCTAACAGTACTGTGTGTAATGGGAGATT 300
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db 301 CGAGTAAGACGCGAGAGAAAGATTTCGCATCAAGTTTCGGTGACTTTTGACATTGAAGATTCT 360
QY 40 GlnThrCysAlaSerAspTyrLeu---LeuPheThrSer-----SerSerAspGln 55
Db 361 GATTATTGTCACTTAATTAATACCTGAAATCTTTAATGGAATTGGAGTCAGACGAAACGAA 420
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 421 ATAGGCAAGTACTGTGTGTTGCTGGTTTACAATGAATCAGTCAATTCAGTCCAAAGGCAGT 480
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 481 GAAATCACAGTGTCTTCATGAGTGAATCCATGCTTCTGGTCAGGATTTTGGGCTTCT 540
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 541 TACTCAGTTATAGATAAACAAGATTTTAATCACTTGTGTGGTACTGTATCTAATTTTGG 600
QY 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 601 GAACCTGAGTTTCAAGTAAAGTACTGCCCGAGCTGGCTGTCTGCTGCTTTTGTCTGAATATCT 660
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaIleHisAla 154
Db 661 GGAACGATTCCTCATGTATAGAGATTCTTCAACCGCTGTGTATGGCTGAATCCATGCA 720
QY 155 GlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
Db 721 GGAGTAGTGTCAAGTGTGGTGGTGGCAATCAGCGTTGTGTATTAGCAAGGCCCAACCCCA 780
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
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Db 781 TATTACGAAAGTCTTTGGCCAAACAATGTCACTTCCATGGTGGGATATCTACGAGT 840
Qy 195 ArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu----- 210
Db 841 CTGTTTACATTTAAGACACTGTGTCTATGGGACTTAGGGATGAGTCAAGTGTGATC 900
Qy 211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValAsnGluSerGlyAspGln 230
Db 901 GCCGATCCCAAGATACAGCATCTGTACTGGAGTGGACTGACCACATGGGCGAGGAG 960
Qy 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db 961 AACAGCTGAAACCCGAGAGGCGAGCTGAGAAAACCGGGGCTCCCTGGGTGCT--- 1017
Qy 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyLysLys 270
Db 1018 TTTGGCAGTATGAGCAT-----CAGTGGCTGCAATTGACCTTAATAGGAGAG 1068
Qy 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTrpValLys 290
Db 1069 AAGATAACAGGCATCTGTAACCACTGGATCTACCTGATAGAGCACAATTACTATGTCT 1128
Qy 291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrTrpLysGlyIleVal 310
Db 1129 GCTACAGAGTTCTGTACAGTGCAGTGGCGAGAAATGGACTGTGTACAGAGCGCTGT 1188
Qy 311 AsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsn 330
Db 1189 GCGGCTCAGCAGAGATATTTCAAGGAACAAGATTATCACAAAGGATGTTGTAATAAC 1248
Qy 331 PheIleProPheValAlaArgTyrValArgValProGlnThrTrpHisGlnArg 350
Db 1249 TTTTGGCCACCAATTATTCAGCTTTTCATTAGATGAACCTCTCCAGTGGCAACAGAA 1308
Qy 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
Db 1309 ATTGCCATAAGTGAATTTGCTGGGATGTCACTTCACTCTGAAAGGTGCGCTTCCAAAG 1368
Qy 364 -----GlnGlyAsnAspSerLeuValTrpArgLysThrSerGln 376
Db 1369 CTTACTCAACCTCCCCACCTCGGAACAGCAATAACCTC-----AAA 1410
Qy 377 SerThrSerValSerThrLys----- 383
Db 1411 AACACTACAGTTTCATCCCAACTAGTCTGCGCCCTAAATTTACTCAAGCACTCCAACCA 1470
Qy 384 -----LysGluAspGluThrIleThrArgProIleProSerGluThrSerThr--- 400
Db 1471 CGAAGTAGGAATGACCTTCTCTG-----CTGCCGCCCCAGACAACCTGCCACTCCT 1521
Qy 401 GlyIleAsnIleThrThr-----ValAlaIleProLeuVal 412
Db 1522 GATGTCAAAAACAGCACTGTGACTCCCACTGTGACCAAAAGATGTGCACTGGCGCGGT 1581
Qy 413 LeuLeuValValLeuValPheAlaGlyMetGlyIlePheAlaAlaPhe----- 428
Db 1582 CTGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1641
Qy 429 -----ArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 1641
Db 1642 CATTTGGAGAAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1698
Qy 445 LysThrAspCysTrpLysGlnIleLys-----TyrProPheAlaArgHisGlnSerAla 462
Db 1699 CGGGCAGGCTGGTGGAAAGAGTGAAGAGTGTCTCCCTCCGCAAAATCGGTGACACAGAG 1758
Qy 463 GluPheThrIleSerTrpAspAsnGlu-----LysGluMetThr 475
Db 1759 GAGACCCAGTGGCTACAGCAACAGTGAAGTTAGTCACTGAGCCCGGAGGAGTCAAG 1818
Qy 476 GlnLysLeuAspLeuIleThrSerAspMetAla 486
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Db 1819 ACAGTGCTGCAAGCTGATTCTCGAGAATACGCA 1851

RESULT 7

US-10-191-436A-9
; Sequence 9, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPT
; TITLE OF INVENTION: UTILITY OF THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-191-436A-9

Alignment Scores:
Pred. No.: 1,24e-87 Length: 2310
Score: 867.50 Matches: 207
Percent Similarity: 54.63% Conservative: 94
Best Local Similarity: 37.57% Mismatches: 171
Query Match: 33.93% Indels: 79
DB: 3 Gaps: 17

US-10-813-588-2 (1-487) x US-10-191-436A-9 (1-2310)

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Qy 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 241 CTTACATCCATCACTCACTCCACATACCTATCTTAACAGTACTGTGTGTAATGGGAGATT 300
Qy 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db 301 CGAGTAAGACGGGAGAGAAGATTGCGATCAAGTTCGGTGACTTGGACATTGAAGATTCT 360
Qy 40 GlnThrCysAlaSerAspTyrLeu---LeuPheThrSer-----SerSerAspGln 55
Db 361 GATTATTGTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
Qy 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 421 ATAGGCAAGTACTGTGGTCTGGGTTTACAAATGAATCAAGTCAATTGAGTCCAAAGCAGT 480
Qy 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 481 GAATACACAGTCTGTTTCATGATGGGATCCATGCTTCTGGTCGAGGATTTTGGCTTCT 540
Qy 95 TyrAlaSerSerAspHisProAspLeuThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 541 TACTCAGTTATAGATAAAACAGATTAAATCACTTGTGGTACTGTATCTAATTTTGG 600
Qy 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 601 GAACCTGAGTTGAGTAAGTACTGCCAGCTGCTGTCTGCTCCCTTTTCTGCTGAAATATCT 660
Qy 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAla 154
Db 661 GGAACGATTCCTCTGATATAGATTTCTTCCCGCTGTGTATGGTGGATTCATGCA 720
Qy 155 GlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
Db 721 GGAGTAGTGTCAAGTGTCTGGTGGCCAAATCAGCGTGTGATTAGCAAAAGCCACCCCA 780
Qy 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
Db 781 TATTACGAAAGTCTTTGGCCCAACAATGTCACTTCCATGGTGGGATACTTATCTACGAGT 840
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QY 195 ArgPheLeuPheThrSerSerLeuGlyCysSerArgSerLeuSerPheGlu----- 210
Db 841 CTGTTTACATTTAAGACAAGTGGTTGCTATGGGACTCTAGGATGGAGTCAGGTGTGATC 900
QY 211 ProAspGlyGlnIleArgAlaSerSerSerTrpGlnSerValAsnGluSerGlyAspGln 230
Db 901 CGCGATCCCGACATAACAGCATATCTGTCTGAGTGAGTACACACATGGGGCAGGAG 960
QY 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db 961 AACAGCTGGAACCCGAGAGCCGAGCTGAGAAACCGGGCTCCCTGGGCTGCT--- 1017
QY 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGlnLysLys 270
Db 1018 TTTGCCACTGATGAGCAT-----CAGTGGCTGCAAAATGACCTTAATAAGGAGAAG 1068
QY 271 LysIleThrGlyIleArgThrGlySerThrGlnSerAsnPheAsnPheThrValLys 290
Db 1069 AAGTAACAGGCATCTGAACCTGATCTTACCTCATAGAGCACATTAATGATGTCT 1128
QY 291 SerPheValMetAsnPheLysAsnAsnAsnSerLysTrpLysThrTrpLysGlyIleVal 310
Db 1129 GCCTACAGAGTCTGTACAGTGACGATGGCGAGAAATGGACTGTGTACAGAGCCCTGT 1188
QY 311 AsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
Db 1189 CGCGCTCAGACAGAATATTTCAAGGAAACAAAGATTATCACAAGGATGTTCGTAAATAAC 1248
QY 331 PheIleProPheValAlaArgTyrValArgValValProGlnThrTrpHisGlnArg 350
Db 1249 TTTTGGCCCAATATGTGACGTTTCATTAGAGTGAACCTGTCCAGTGGCAACAGAAA 1308
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
Db 1309 ATTGCCATGAAGTGAATTTGCTGGGATGTCACTCTGAAGGTGCGCTTCCAAAG 1368
QY 364 -----GlnGlyAsnAspSerLeuValTrpArgLysThrSerGln 376
Db 1369 CTTACTCAACCTCCCGCACCTCGGACAGCAATACCTC-----AAA 1410
QY 377 SerThrSerValSerThrLys----- 383
Db 1411 AACACTACATTTATCCCAAACTAGTGTGCGCCCTAAATTTACTCAAGCACTCCCAACCA 1470
QY 384 -----LysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr--- 400
Db 1471 CGAAGTAGGAATGACCTTCCTCTG-----CTGCGCGCCCGACAGCAACTGCCACTCCT 1521
QY 401 GlyIleAsnIleThrThr-----ValAlaIleProLeuVal 412
Db 1522 GATGTCAAAAACACGACTGTGACTCCCGAGTGTGACCACAAAGATGTGCACCTGGCGCGGTT 1581
QY 413 LeuLeuValValLeuValPheAlaGlyMetGlyIlePheAlaAlaPhe----- 428
Db 1582 CTGGTTCCTGTGCTGTGTCATGGCCCTCACCACACTCATCTCTCATCTTAGTGTGTCTGG 1641
QY 429 -----ArgLysLysLysLysLysGlySerProTyrGlySerAlaGluAlaGln 444
Db 1642 CATTGGAGAAACAGAAAGAAAGCCGAGGACCC---TATGATTATACCCCACTGGAT 1698
QY 445 LysThrAspCysTrpLysGlnIleLys-----TyrProPheAlaArgHisGlnSerAla 462
Db 1699 CGGGCAGCGCTGGTGAAGAGGAGTGAAGCAGCTTCTCCCTGCCAAATCGGTGGAAACAGAG 1758
QY 463 GluPheThrIleSerTyrAspAsnGlu-----LysGluMetThr 475
Db 1759 GAGACGCCATGGCTACAGCAACAGTGAAGTTAGTCACTGACCCCGAGGAGTCAAG 1818
QY 476 GlnLysLeuAspLeuIleThrSerAspMetAla 486
Db 1819 ACAGTGCTGCAAGCTGATTCTGCAGAAATACGCA 1851
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RESULT 8

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US-10-191-436A-1
; Sequence 1, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiko Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(198)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (199)..(2328)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2328)
US-10-191-436A-1
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Alignment Scores:
Pred. No.: 7,79e-87 Length: 2328
Score: 860.50 Matches: 206
Percent Similarity: 54.33% Conservative: 95
Best Local Similarity: 37.18% Mismatches: 170
Query Match: 33.65% Indels: 83
DB: Gaps: 17
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US-10-813-588-2 (1-487) x US-10-191-436A-1 (1-2328)

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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 250 CTTACATCCATAAACTACCCACAGACCTATCCCAACAGCACCTGTTGTGAATGGGAGATC 309
QY 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db 310 CGTGTAAAGATGGGAGAGAGATTCGCATCAAAATTTGGTGACTTTGACATTGAAGATTCT 369
QY 40 GlnThrCysAlaSerAspTyrLeuLeuPheThrSer-----SerSerAspGln 55
Db 370 GATTCCTGTGCTACTTTAATTTACTTTGAGAAATTTAATGGAATGGAGTCAGCAGAACTGAA 429
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 430 ATAGGCAATATCTGTGCTGGGTTGCAAAATGAACCAATTCATTTGAATCAAAAGGCAAT 489
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 490 GAAATCACATTCGTGTTCATGATGGAATCCATGTTCTGGACGCGGATTTTGGGCTCA 549
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 550 TACTCTGTTATAGATAAACAAGATCTAATTAATCTTTGTGGACACTGCATCCCAATTTTGG 609
QY 115 LysThrGluLysSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 610 GAACCTGAGTTCAGTAAGTACTGCCAGCTGGTGTGCTCTCTCTCTCTCTCTCTCTCTCT 669
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaIleHisAla 154
Db 670 GGAACAAATTCCTCATGATATAGAGATTCCTGCCCATTTGTGATGCTGGTGTGCAATGCA 729
QY 155 GlyIleIleAlaAspGluLeuGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
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Db 730 GGAGTAGTGTCAACACAGCTTTGGCGCCAAATCAGTGTGTGTAATTAAGTAAAGGTATTCCC 789
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
Db 790 TATTATGAAGTCTTTGGCTTAACACGTCACATCTGTGTGGGACACATTATCTACAGT 849
QY 195 ArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu----- 210
Db 850 CTTTTTACATTTAAGACACAGTGTATGAACACCTGGGATGGAGTCTGTGTGATC 909
QY 211 ProAspGlyGlnIleArgAlaSerSerThrGlnSerValAsnGluSerGlyAspGln 230
Db 910 GCGGATCCTCAATAACACAGCATCTCTGCTGGAGTGGACTCACCACACAGGCGAAG 969
QY 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db 970 AACAGTTGGAAACCCAAAAAGCGAGCTGAAAAACCTGGACCGCTTGGGCTGCTTTT 1029
QY 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGlyLys 270
Db 1030 GCCACTGATGAA-----TACCAGTGGTTACAAATAGATTGTAATAAGGAAAG 1077
QY 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheThrValLys 290
Db 1078 AAAATAACAGGCAATTATAACCACTGGATCCACCATGGTGAGCACAATTAATCTATGTGCT 1137
QY 291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrTyrLysGlyIleVal 310
Db 1138 GCCTCAGATCTCTGACAGTGTATGATGGCAGAAATGACTGTGTACAGAGCCTGGT 1197
QY 311 AsnAsnGluGlyLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
Db 1198 GTGGAGCAAGATAAGATATTCAAGGAAACAAAGATTATCACCAGGATGTGCGTAATAAC 1257
QY 331 PheIleProPheValAlaAlaArgTyrValArgValProGlnThrTrpHisGlnArg 350
Db 1258 TTTTTCGCCCAATATTGACGCTTTATTAGAGTGAATCTTACCCTACCGAGCAGAA 1317
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGln----- 361
Db 1318 ATTGCCATGAATGAGCTGTCTGGATGTCACTTTATTCCTTAAGGTGTCTCTCAAAA 1377
QY 362 IleThrGln-----GlyAsnAspSerLeuValTrpArgLysThrSer 375
Db 1378 CTTACTCAACCTCCACCTCTCTCGAACACAGCAATGAC-----CTCAAAACACT 1425
QY 376 GlnSerThrSerValSerThrLysLysGluAspGluThrIleThrArgProIle----- 393
Db 1426 ACAGCCCCCTCAAAAATAGCAAAAGTCTGTGCCCCAAAATTTACGCAACCACTACAACT 1485
QY 394 -----ProSerGluGluThr-----SerThrGlyIleAsn 403
Db 1486 CGCAGTAGCAATGAATTTCTGTGCACAGACAGAAACAACAACTGCCAGTCTGTATATCAGA 1545
QY 404 IleThrThr-----ValAlaIleProLeuValLeuVal 415
Db 1546 AATACTACCGTAACCTCAAAATGTAACCAAGATGTAGCGTGGCTGCAGTCTCTGTCCCT 1605
QY 416 ValLeuValPheAlaGlyMetGlyIlePheAlaAlaPhe----- 428
Db 1606 GTGCTGGTCAATGCTCCTCACTCTCTCAATTTCTCATATTAGTGTGTGCTTGGCAGCTGAGA 1665
QY 429 ---ArgLysLysLysLysLysGlySer-----ProTyrGlySerAlaGluAlaGln 444
Db 1666 AACAGAAAGAAAAAAGAACTGAGGACCACTTATGACTTACCTTACTGG-----GAC 1713
QY 445 LysThrAspCysTrpLysGlnIleLysTyr----- 454
Db 1714 CGGGCAGGTTGGTGGAAAGAAAGAAAGAGCAGTCTTCTTCTGCAAAAGCAGTGACCATGAG 1773
QY 455 -----ProPheAlaArgHisGlnSerAlaGluPheThrIleSerTyrAspAsnGluLys 472
Db 1774 GAAACCCCA---GTTCTGCTATAGCAGCAGCGAA-----GTTAATCACCCTGAGTCCAAGA 1824

QY 473 GluMetThrGlnLysLeuAspLeuIleThrSerAspMetAla 486
Db 1825 GAAGTCACACAGTGTCTGAGGCTGACTGTGCAGAGTATGCT 1866

RESULT 9

US-10-191-436A-3
; Sequence 3, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDM, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-436A-3

Alignment Scores:

Pred. No.: 7,79e-87 Length: 2328
Score: 860.50 Matches: 206
Percent Similarity: 54.33% Conservative: 95
Best Local Similarity: 37.18% Mismatches: 170
Query Match: 33.65% Indels: 83
DB: 3 Gaps: 17

US-10-813-588-2 (1-487) x US-10-191-436A-3 (1-2328)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGlyLysThrIle 20
Db 250 CTTACATCCATAAACTACCCACAGACCTATCCACAGCAGCTGTTGTGAATGGGAGATC 309
QY 21 ThrValProLysGlyLysArgLeuLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db 310 CGTGTAAAGATGGGAGAGAGAGTTCGCATCAAAATTTGGTGACTTTGCATTTGAAGATTCT 369
QY 40 GlnThrCysAlaSerAspTyrLeuLeuPheThrSer-----SerSerAspGln 55
Db 370 GATTCCTGTCACTTAAATTACTTGAGAAATTAATGAATTTGGAGTTCAGCAGAACTGAA 429
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 430 ATAGGCAATACTGTGGTCTGGGGTTGCAAAATGAACCATTTCAATTGAATCAAAAGCAAT 489
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 490 GAAATCACATTCCTCTGTTCATGATGGAATCCCATGTTCTGGACGGGATTTTGGCCTCA 549
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 550 TACTCTGTATAGATAAAACAAGATCTAATTAATTTGTTGGACACTGCATCCCAATTTTGG 609
QY 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 610 GAACTGTAGTTCAGTAAGTACTGCCAGCTGTTGTCTGCTCTCTCTCTCTCTCTCTCTCT 669
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysGlyAlaAlaIleHisAla 154
Db 670 GGAACAATTCCTCATGATATAGAGATTCCTCGCCATTTGTGATGCTGCTGCTGCTGCTG 729
QY 155 GlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
Db 730 GGAGTAGTGTCAACACAGTGTGGCGCCAAATCAGTGTGTGTAATTAAGTAAAGGTATTCCC 789
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194

Db	790	TATTATGAAAGTCTTTGGCTTAACAACGTCACATCTGTGTGGGACACATTTATCTACAAGT	849
Qy	195	ArgPheLeuPheThrSerAenGlyCySeSerArgSerLeuSerPheGlu	210
Db	850	CTTTTTCATTTAAGACACAGTGGATGTATGGAACACTGGGGATGGAGTCTGGTGTGATC	909
Qy	211	ProAspGlyGlnIleArgAlaSerSerSerTrpDlnSerValAenGluSerGlyAspGln	230
Db	910	CGCGATCCTCAAAATAACAGCATCATCTGTCTGGAGTGGACTGACCACACAGGGCAAGAG	969
Qy	231	ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly	250
Db	970	AACAGTTGGAAACCCCAAAAGCCAGGCTGAAAAACCTGGACCGCTTGGGCTGCTTTT	1029
Qy	251	AspSerSerAenAenHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLysLys	270
Db	1030	GCCCATGATGAA-----TACAGTGGTTACAAATAGATTTGAATATAGGAAAG	1077
Qy	271	LysIleThrGlyIleArgThrGlySerThrGlnSerAenPheAenPheTyrValLys	290
Db	1078	AAATAACAGGCATTATAACCACTGGATCCACCATGGTGGAGCACATTAATACTATGTCT	1137
Qy	291	SerPheValMetAenPheLysAenAenAenSerLysTrpLysThrTyrLysGlyIleVal	310
Db	1138	GCCTACAGAATCTCTGTACAGTGATGCGGCAGAAATGGACTGTGTACAGAGAGCCTGGT	1197
Qy	311	AsnAenGluLysValPheGlnGlyAenSerAenPheAenPheArgAspProValGlnAenAsn	330
Db	1198	GTGGAGCAGAGATAAGATATTTCAGGAAACAAAGATATATCCAGGATGCGGTAAATAC	1257
Qy	331	PheIleProPheValAlaIleArgValArgValValProGlnThrTrpHisGlnArg	350
Db	1258	TTTTTGGCCAAATATTTCACGTTTATTAGAGTGAATCTTACCCCAATGCGCAGCAGAAA	1317
Qy	351	IleAlaLeuLysValGluLeuIleGlyCysGln-----	361
Db	1318	ATTGCCATGAAATGGAGCTGCTCGGATGTCAGTATTCTCTAAAGGTCGCTCTCCAAAA	1377
Qy	362	IleThrGln-----GlyAenAspSerLeuValTrpArgLysThrSer	375
Db	1378	CTTACTCAACTCCACCTCTCTGGAGCAGCAATGAC-----CTCAAAACACT	1425
Qy	376	GlnSerThrSerValSerThrLysLysGluAspGluThrIleThrArgProIle-----	393
Db	1426	ACAGCCCTCCAAAATAGCCAAAGGTCGTGCCCCAAAATTTACGCAACCACTACACCT	1485
Qy	394	-----ProSerGluGluThr-----SerThrGlyIleAsn	403
Db	1486	CGCAGTAGCAATGAATTTCTTCGCACAGACAGACAAACAACTGCGCAGTCTGTATCAGA	1545
Qy	404	IleThrThr-----ValAlaIleProLeuValLeuVal	415
Db	1546	AATACTACCGTAATCCAAATGTAAACCAAGATGTAGCGCTGGCTGAGTCTTGTCCCT	1605
Qy	416	ValLeuValPheAlaGlyMetGlyIlePheAlaIlePhe-----	428
Db	1606	GTGCTGGTCATGGTCCCTCACTACTCTCATTTCTATATTAGTGTGTGTGGCACTGGAGA	1665
Qy	429	---ArgLysLysLysLysLysGlySer-----ProTyrGlySerAlaGluAlaGln	444
Db	1666	AACAGAAAGAAAAAATCGAAGGCCACCTATGACTTACCTTACTCG-----GAC	1713
Qy	445	LysThrAspCysTrpLysGlnIleLysTyr-----	454
Db	1714	CGGCGAGGTGCTGGAAAGGAATGAAGCAGATTTCTTCTGCAAAAGCAGTGGACATGAG	1773
Qy	455	-----ProPheAlaArgHisGlnSerAlaGluPheThrIleSerTyrAspAsnGluLys	472
Db	1774	GAAACCCCA---GTTTCGTATAGCAGCAGCAA-----GTTATCATCCTGAGTCCAAGA	1824
Qy	473	GluMetThrGlnLysLeuAspLeuIleThrSerAspMetAla	486

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QY 155 GlyIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
Db 721 GGAGTAGTCAAAAGTGTGGTGGCCCAATCAGCATTTGTATTAGCAAGAGACCCCA 780
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
Db 781 TATTATGAAGAGCTCTTTGGCCAAATGTCACCTCCACGGTGGGATCTTATCTGCAAGT 840
QY 195 ArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu----- 210
Db 841 CTGTTTACATTTAAGCAAGTGTGCTATGGAGCTCTGGGATGGAGTCTGGTGTGATT 900
QY 211 ProAspGlyGlnIleArgAlaSerSerTyrGlnSerValAsnGluSerGlyAspGln 230
Db 901 GCCGATCCCAAGATACAGATCGTCTGACCTGGAGTGACTGACACATGGGCGAGAG 960
QY 231 ValHisTyrSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTyrAlaSerGly 250
Db 961 AACAGCTGCACAGCGGAGGAGCGAGCTGAGAAACCCGGGCTCCCTGGGCTGCT--- 1017
QY 251 AspSerSerAsnAsnHisLysProArgGluTyrLeuGluIleAspLeuGlyLys 270
Db 1018 TTTGCCACGTGATGAGCAT-----CAGTGGCTGCAGATAGACCTTAACAAGGAGAAG 1068
QY 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLys 290
Db 1069 AAGATTAACAGGTATCTGTAACCACTGGTGTACCATGATAGACACAGTTACTATGTGCT 1128
QY 291 SerPheValMetAsnPheLysAsnAsnSerLysTyrLysThrTyrLysGlyIleVal 310
Db 1129 GCCTACAGAGTCTGTACAGTGACGATGGCAGAGATGGACTGTGTACAGAGAACCTGTT 1188
QY 311 AsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
Db 1189 GTGGACCGACGACAAGATATTTCAAGGAAACAAAGATTATCACAAAGGATGTTGCTATAAC 1248
QY 331 PheIleProPheValAlaAlaArgTyrValArgValValProGlnThrTyrHisGlnArg 350
Db 1249 TTTTTCGCCAACCAATTATTCAGCTTTTCAATTAGAGTGAAACCTGTCCAGTGGGCACAGAAA 1308
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
Db 1309 ATTGCCATGAAGTGAAGTCTGCTCGATGTGCTGCTCAAAAGTGCCTTCCAAAG 1368
QY 364 -----GlnGlyAsnAspSerLeuValTyrArgLysThrSer----- 375
Db 1369 CTTACTCCACCTCTCCGGAACGCAATAAC-----CTCAGAAATACTACAGCTCGT 1419
QY 376 -----GlnSerThr 378
Db 1420 CCCAACTAGGTAAAGGTGTGGCCCTAAATTTACTCAAGTGTCCAACTCGAAGTAGG 1479
QY 379 SerValSerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThr 398
Db 1480 AATGAACCTCTCTGTCAGCGCGGAGACAACTACCCTCTGTATATAAAACACAGACT 1539
QY 399 SerThrGlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuVal 418
Db 1540 GTAACCTCCCAAGTAAACCAAGATGTGCACCTGGCTGCCGCTTCTGCTCCCTGTGCTGTC 1599
QY 419 PheAlaGlyMetGlyIlePheAlaAlaPhe-----ArgLys 430
Db 1600 ATGGCCCTCACCACTCATCTCTATTCTAGTGTGTGGCTGGCAGTGGAGAACAGAGAG 1659
QY 431 LysLysLysLysGlySerProTyrGlySerAlaGluAlaGlnLysThrAspCysTyrLys 450
Db 1660 AAGAAACTGAAGCGCC---TATGATTTACCCCACTGGGATCGGCGAGTTGGTGGAAA 1716
QY 451 GlnIleLysTyrProPhe-----AlaArgHis 459
Db 1717 GGAATGAAGCAGCTTCTCCCTGCCAAGTGGTGGACCAAGGAGAGCGCCAGTGCCTAC 1776
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QY 460 GlnSerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAsp 479
Db 1777 ACACATAGTGA-----GTCACTCACCTGAGTCCGAGGGAAGTACCACAGTGTGTCAG 1830
QY 480 LeuIleThrSerAspMetAla 486
Db 1831 GCCGACTCTGCAGAAATATGCA 1851
RESULT 11
US-10-191-436A-6
; Sequence 6, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPT
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-191-436A-6
Alignment Scores:
Pred. No.: 2,18e-86 Length: 2310
Score: 856.50 Matches: 203
Percent Similarity: 54.66% Conservative: 96
Best Local Similarity: 37.11% Mismatches: 177
Query Match: 33.50% Indels: 71
DB: 3 Gaps: 14
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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 241 CTTATCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 300
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyValAspLeuAspIleGlu---Ser 39
Db 301 CGAGTCAGACCGGAGAGAGAGATTGCATCAAAATTCGGTGACTTTGACATTGAAGATTCT 360
QY 40 GlnThrCysAlaSerAspTyrLeu---LeuPheThrSer-----SerSerAspGln 55
Db 361 GATTATTGTACCTTAATTTACCTGAAATCTTTAATGGAATTTGGAGTCAGACAGACGAA 420
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 421 ATAGGCAAAATACTGTGGTCTGGGTTTACAAATGAATCAGTCAATGAGTCCAAAGCAGT 480
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 481 GAAGTCACAGTCTGTTTATGATGGAGACCCATGCTGCTGGCGAGGATTTTGGCTTCA 540
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 541 TACTCAGTTATAGATAAAGAAGATTAAATCACTTGTGATGATCTGTCTAATTTTGTG 600
QY 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 601 GAACCAAGATTCAGTAAGTACTGCCAGCTGCTGCTTTTGGCTTTTGTCTGAAATATCT 660
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAla 154
Db 661 GGAACAAATTCCTCATGATACAGAGATTCTTCCCAATTTGTATGCTGGAATCCATGCA 720
QY 155 GlyIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
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Db 721 GGAGTAGTGCAAACTGGTGGTGCCCAATCAGCATTTGTGATTAGCAAAAGGAGCCCA 780
Qy 175 ArgTyrGluGlyIleLeuAlaAenglyValLeuSerArgAspGlySerLeuSerAspLys 194
Db 781 TATTATGAAGCTCTTTGGCCAAACATGTCTCCACGGTGGGATCTATCTGCAAGT 840
Qy 195 ArgPheLeuPheThrSerAenglyCysSerArgSerLeuSerPheGlu----- 210
Db 841 CTGTTTACATTTTAAGACAAGTGTCTATGGGACTCTGGGGATGGAGTCTGTGTGATT 900
Qy 211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValAendGluSerGlyAspGln 230
Db 901 GCGGATCCCGAGTAACAGCATGCTCTGCATGGAGTGAGTACACACATGGGGCAGGAG 960
Qy 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db 961 AACAGCTGGACAGCGGAGGAGCCGCTGAGAAACCCGGGCTCCCTGGGCTGCT--- 1017
Qy 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyLysLys 270
Db 1018 TTTGCCACTGATGAGCAT-----CAGTGGCTGCAGATAGACCTTAACAGGAGAAG 1068
Qy 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLys 290
Db 1069 AAGTAACAGGTATCTTAACCTCTGGTCTTACATGATAGAACACAGTACTATGTGTCT 1128
Qy 291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrTyrLysGlyIleVal 310
Db 1129 GCCTACAGAGTCTGTACAGTACGATGGCGACAGATGGACTGTGTACAGAGAACCTGTT 1188
Qy 311 AsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
Db 1189 GTGGACGAGCAAGATATTTCAAGGAAACAAAGATTATCACAAGGATGTTCTGTAATAAC 1248
Qy 331 PheIleProPheValAlaAlaArgTyrValArgValProGlnThrTrpHisGlnArg 350
Db 1249 TTTTGGCCCAATTATTCACGCTTTTCATTAGAGTGAACCTCTCCAGTGGCAACAGAAA 1308
Qy 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
Db 1309 ATTGCCATGAAGTGGAACTGCTCGGATGTCAGTTTACTCTCAAGTGCCTTCACAAAG 1368
Qy 364 -----GlnGlyAsnAspSerLeuValTrpArgLysThrSer----- 375
Db 1369 CTTACTCCACTCTCTCGAACCGCAATAAC-----CTCAGAAATACTACAGCTCGT 1419
Qy 376 -----GlnSerThr 378
Db 1420 CCCAACTAGTAAAGTGTGCGCCCTAAATTTACTCAAGTGTCTCCACCTCGAAGTAGG 1479
Qy 379 SerValSerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThr 398
Db 1480 AATGAACCTCTGTGCAGCGCGGAGACAACTACCACTCTGATATAAAAAACAGACT 1539
Qy 399 SerThrGlyIleAsnIleThrValAlaIleProLeuValLeuValValLeuVal 418
Db 1540 GTAACCTCCAGTGTAAACAAAGATGTCCGACTGGCTGCGCTTCTGGTCTGCTGGTGC 1599
Qy 419 PheAlaGlyMetGlyIlePheAlaAlaPhe-----ArgLys 430
Db 1600 ATGGCCCTCACCACACTCATCTCTAGTGTGTGCTGGCACTGGAGAACACAGGAAG 1659
Qy 431 LysLysLysLysGlySerProTyrGlySerAlaGluAlaGlnLysThrAspCysTrpLys 450
Db 1660 AAGAAAACCTGAAGCGGC---TATGATTATCCCACTGGGATCGGGCAGGTGTGTGGAAA 1716
Qy 451 GlnIleLysTyrProPhe-----AlaArgHis 459
Db 1717 GGAATGAAGCAGCTTCTCTCCCTGCAAGTGGTGGACCAAGAGAGAGCGCAGTGGCGCTAC 1776
Qy 460 GlnSerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAsp 479
Db 1777 AGCACTAGTGAA-----GTCACTCAGTGCAGGGAAGTCAACACAGTGTCTGCAG 1830

Qy 480 LeuIleThrSerAspMetAla 486
Db 1831 GCCGACTCTGCAGAAATATGCA 1851
RESULT 12
US-09-116-473-1
; Sequence 1, Application US/09116473
; Patent No. 6428965
; GENERAL INFORMATION:
; APPLICANT: Kolodkin, Alex
; APPLICANT: Ginty, David
; TITLE OF INVENTION: SEMAPHORIN RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/116,473
; FILING DATE: 17-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/052,762
; FILING DATE: 17-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107,74973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-116-473-1
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Pred. No.: 1.45e-26 Length: 3371
Score: 331.50 Matches: 112
Percent Similarity: 40.13% Conservative: 73
Best Local Similarity: 24.30% Mismatches: 174
Query Match: 12.96% Indels: 102
DB: 3 Gaps: 17
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Db 429 ATCACTTCCCGAGGTATCCCGCAGGACTATCCCTCTCACAGNACTGTAGTGGTGTGC 488
Qy 21 ThrValProLys---GlyLysArgLeuIleLeuArgLeuGly---AspLeuAspIleGlu 38
Db 489 TATGCCCGCCGACCCCAACCAAGAGATTGTCTCAACTTCAACCCCTCACTTTGAAATCGAG 548
Qy 39 SerGlnThrCysAlaSerAspTyrLeuLeuPhe-----ThrSerSerSerAsp 54
Db 549 AAGCATGACTGCAAGTATGACTTTCATTGAGATTCGGAGTGGAGACAGTGAAGTCAAGTGC 608
Qy 55 GlnTyrGlyProTyrCysGlySerMetThrValProLysGluLeuLeuLeuAsnThrSer 74


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QY 122 -----CysProAlaGlyCysArgAspValAlaGlyAsp 132
Db 595 GACCTTTTCAGCTGGAGAGGGGAGTCTGCAAGTAGATTGGCTGACATCTGGGATGGC 654
QY 133 IleSer-----GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysIysAla 150
Db 655 ATCCACATGTTGGCCCTCTGATGTCAGTGTGGGACCAAAACACCTCTGAACTT 714
QY 151 AlaIleHisAlaGlyIleAlaAspGluLeuGlyGlnIleSerValLeuGluArg 170
Db 715 CGTTCAATCAGCGGGATCTCTCCCTGACCTTTCACACGACATCGCGTGGCCAAAG--- 771
QY 171 LysGlyIleSerArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySer 190
Db 772 -----GATGGCTTCTCTGCGCTTACTACTCTGTCTCCACCAAGAGCCA 813
QY 191 LeuSerAspLysArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu 210
Db 814 CTAGAGAACTTTCAG-----TGCAATGTTCTCTGGCGCATGGAG 852
QY 211 -----ProAspGlyGlnIleArgAlaSerSerTyrProlGlnSerValaGlu 226
Db 853 TCTGGCCGATTCCTAATGAACAGATCAGTGCCTCATCTACCTAC----- 897
QY 227 SerGlyAspGlnValHisTyrSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSer 246
Db 898 -----TCTGATGGAGGTGGACCTCAACAAAGCGGCTCATCGTGTGATGACATGGC 951
QY 247 TrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGluTrpLeuGluLeuAspLeu 266
Db 952 TGGACCCCAACTTGGATTTCCAAAC-----AAGAGTATCTCCAGGTGGACCTG 999
QY 267 GlyGluLysLysIleThrGlyIleArgThrThrGly-----SerThrGlnSerAsn 284
Db 1000 CGCTTTTAAACATGCTCAGCGCATCGCAACACAGGAGCGCATTTCCAGGGAAACACAG 1059
QY 285 PheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnSerLysTrpLys 304
Db 1060 AATGGCTACTAGTCAATCTACAGCTGGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1119
QY 305 ThrTyrLysGlyIleValaAsnAsnGluLysValPheGlnGlyAsnSerAsnPheArg 324
Db 1120 GTGTACCGGCATGGCAAAACACAC-----AAGGTATTTCAAGCCCAACATGCAACT 1173
QY 325 AspProValGlnAsnAsnPheIleProProlIleValaAlaArgTyrValArgValValPro 344
Db 1174 GAGGTGGTTCTGAACCAAGCTCCACGCTCCACTGCTCAACAGGTTTGTAGAATCCGCCT 1233
QY 345 GlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGln 364
Db 1234 CAGACTTGCACCTCAGGTATCGCCCTCCGGCTGGAGCTCTTCGGCTGCGGGTCAAGAT 1293
QY 365 GlyAsnAspSer-LeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLys 384
Db 1294 GCTCCCTGCTCCAAACATGCTGG-----GGATGCTCTCAGGCTCATTCAGACTCCCGAG 1347
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Db 1348 A-----TCTCCGCTCTTCCACCCAGGAATACCTCT 1378

RESULT 15
US-08-936-135-19
; Sequence 19, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Teesier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
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; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-936-135-19

Alignment Scores:
Pred. No.: 1-77e-26 Length: 2781
Score: 329.50 Matches: 113
Percent Similarity: 40.78% Conservatives: 73
Best Local Similarity: 24.78% Mismatches: 178
Query Match: 12.89% Indels: 92
DB: 3 Gaps: 18

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QY 21 ThrValProLys--GlyLysArgLeuLeuLeuArgLeuGly--AspLeuAspIleGlu 38
Db 178 TAGCCCCCGAACCACCAAGAGATTGTCTCAACTTCAACCTCATTGAAATCGAG 237
QY 39 SerGlnThrCysAlaSerAspTyrLeuLeuPhe-----ThrSerSerSerAsp 54
Db 238 AAGCAGCATTCGAAGTATGACTTTATCGAGATTCGGGATCGGACAGTGAATCCGACAG 297
QY 55 GlnTyrGlyProTyrCysGlySerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 298 CTCCTGGGCAACACTGTGGGAATC---GCCCGCCCAACCATCATCTCTCGGGCTCC 354
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 355 ATGCTTACATCAAGTTTCACTCCGACTACGCCCGGAGGGGGGAGGCTTCTCTCTGCGC 414
QY 95 Tyr-----AlaSerSerAsp----- 99
Db 415 TACGAGATCTTCAAGACAGGCTCTGAGATTCTCAAAAACTTCAAGCCCCCAACGGG 474
QY 100 -----HisProAspLeuIleThrCys----- 106
Db 475 ACCATCGAATCTCTGGGTTTCTCGAAGATATCCACAACTTGGACTGCACCTTTTACC 534
QY 107 ---LeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLysPhe----- 121
Db 535 ATCTGGGCAAAACCAAGATGGAGATCTCTGCGAGTTCTCTGATCTTCACTGAGCAT 594
QY 122 -----CysProAlaGlyCysArgAspValAlaGlyAsp 132
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Db      595  GACCCCTTTCAGGTGGAGAGGGGAGCTGCAAGTACGATTGGCTGACATCTGGGATGGC 654
Qy      133  ILeSer-----GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAla 150
Db      655  ATTCCACATGTTGGCCCCCTGATTGGCAAGTACTGTGGGACCAAAACACCCCTCTGAAC TT 714
Qy      151  AlaIleHisAlaGlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArg 170
Db      715  CGTTTCATCGACGGGGATCTCTCCCTGACCTTTCCACGCGCATGGCGGTGGCCAAG--- 771
Qy      171  LysGlyIleSerArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySer 190
Db      772  -----GATGGCTTCTCTGGCGGTACTACTCTGTCACCAAGAGCCCA 813
Qy      191  LeuSerAspLysArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu 210
Db      814  CTAGAGAACTTTCAG-----TGCAATGTTCTCTGGGCATGGAG 852
Qy      211  -----ProAspGlyGlnIleArgAlaSerSerSerTrpGlnSerValAsnGlu 226
Db      853  TCTGGCCGGATTGCTAATGAACAGATCAGTGCCTCATCTACCTAC----- 897
Qy      227  SerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSer 246
Db      898  -----TCTGATGGGAGGTGGACCCCTCAACAAGCCGGCTCCATGGTGATGACAATGGC 951
Qy      247  TrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeu 266
Db      952  TGGACCCCAACTTGGATCCAC-----AGGAGTATCTCCAGGTGGACCTG 999
Qy      267  GlyGluLysLysLysIleThrGlyIleArgThrGly-----SerThrGlnSerAsn 284
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Qy      285  PheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnSerLysTrpLys 304
Db      1060  AATGGCTACTACTCAATCTCAAGCTGGAAGTCAGCACTAATGGAGGAGGACTGGATG 1119
Qy      305  ThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArg 324
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Qy      325  AspProValGlnAsnAsnPheIleProPheIleValAlaArgTyrValArgValPro 344
Db      1174  GAGGTGGTTCTGAACAAGCTCCACGCTCCACTGCTGACAAAGGTTGTAGAAATCCGCCCT 1233
Qy      345  GlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGln 364
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Qy      365  GlyAsnAspSer-LeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLys 384
Db      1294  GCTCCCTGCTCCAAACATGCTGG-----GGATGCTCTCAGGCCTCATTCGACACTCCAG 1347
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Db      1348  A-----TCTCCGCTCTTCCACCAGGAATACCTCT 1378
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Job time : 278 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 20:06:18 ; Search time 387 Seconds
(without alignments)
1018.482 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10813588 @CGN 1.184 @runat_12012006_171133_15476
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New.*
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3: /cn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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6: /cn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /cn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /cn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
9: /cn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
10: /cn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	331.5	13.0	3371	7	US-11-136-527-2829
2	321	12.6	6914	7	US-11-136-527-2829
3	298	11.7	3471	7	US-11-136-527-533
4	285.5	11.2	1400	7	US-11-128-061-3655
5	285.5	11.2	4374	7	US-11-128-061-13
6	285.5	11.2	4999	6	US-10-632-645-14
7	285.5	11.2	11933	6	US-10-632-645-13
8	280	11.0	452	7	US-11-136-527-989

9	280	11.0	452	7	US-11-136-527-5085	Sequence 5085, Ap
10	217	8.5	3935	6	US-10-947-249-162	Sequence 162, App
11	184.5	7.2	3772	6	US-10-131-826A-391	Sequence 391, App
12	174	6.8	2205	7	US-11-137-465-32	Sequence 32, Appl
13	174	6.8	2719	6	US-10-652-893-1	Sequence 1, Appl1
14	169.5	6.6	4960	7	US-11-150-883-49	Sequence 49, Appl
15	169	6.6	2521	7	US-11-128-061-787	Sequence 787, Appl
16	163.5	6.4	2460	7	US-11-150-883-4	Sequence 4, Appl1
17	159	6.2	2091	7	US-11-150-883-53	Sequence 53, Appl
18	156.5	6.1	2595	6	US-10-995-561-90	Sequence 90, Appl
19	156.5	6.1	8957	6	US-10-995-561-89	Sequence 89, Appl
20	156.5	6.1	9040	6	US-10-995-561-91	Sequence 91, Appl
21	155.5	6.1	2924	7	US-11-136-527-1860	Sequence 1860, Ap
22	155	6.1	8409	6	US-10-995-561-13494	Sequence 13494, A
23	154.5	6.0	2090	7	US-11-150-883-50	Sequence 50, Appl
24	153	6.0	1510	6	US-10-947-249-97	Sequence 97, Appl
25	146.5	5.7	2961	7	US-10-821-234-458	Sequence 458, App
26	144.5	5.7	2711	7	US-11-128-061-3312	Sequence 3312, Ap
27	141.5	5.5	11920	6	US-10-995-561-76	Sequence 76, Appl
28	141	5.5	1379	6	US-10-750-185-30427	Sequence 30427, A
29	141	5.5	1379	6	US-10-750-623-30427	Sequence 30427, A
30	140.5	5.5	2773	7	US-11-102-240-33	Sequence 33, Appl
31	140.5	5.5	5383	7	US-11-136-527-3073	Sequence 3073, Ap
32	139	5.4	5293	7	US-11-000-688-1101	Sequence 1101, Ap
33	136.5	5.3	1612	6	US-10-453-372-101	Sequence 101, App
34	136.5	5.3	2106	6	US-10-453-372-85	Sequence 85, Appl
35	136.5	5.3	2268	6	US-10-453-372-81	Sequence 81, Appl
36	136.5	5.3	2268	6	US-10-453-372-103	Sequence 103, App
37	136.5	5.3	2268	6	US-10-453-372-105	Sequence 105, App
38	136.5	5.3	2268	6	US-10-453-372-107	Sequence 107, App
39	136.5	5.3	2268	6	US-10-453-372-109	Sequence 109, App
40	136.5	5.3	2268	6	US-10-453-372-111	Sequence 111, App
41	136.5	5.3	2272	6	US-10-453-372-99	Sequence 99, Appl
42	136.5	5.3	2280	6	US-10-453-372-83	Sequence 83, Appl
43	136.5	5.3	2305	6	US-10-453-372-87	Sequence 87, Appl
44	136.5	5.3	2400	6	US-10-453-372-91	Sequence 91, Appl
45	136.5	5.3	2403	6	US-10-453-372-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1

US-11-136-527-2829
; Sequence 2829, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2829
; LENGTH: 3371
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2829

Alignment Scores:
Pred. No.: 1.46e-25 Length: 3371
Score: 331.50 Matches: 112
Percent Similarity: 40.13% Conservative: 73
Best Local Similarity: 24.30% Mismatches: 174
Query Match: 12.96% Indels: 102
DB: 7 Gaps: 17

US-10-813-588-2 (1-487) x US-11-136-527-2829 (1-3371)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20


```
Qy 397 luThrSerThrGlyIleAanIleThrThrValalaIleProLeu 411
|||||
Db 1503 AGACAGAACTGGATGCCAGAAACATCCGCTGGTGACCACTC 1546
|||||

RESULT 4
US-11-128-061-3655
; Sequence 3655, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3655
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-128-061-3655

Alignment Scores:
Pred. No.: 5,02e-21 Length: 1400
Score: 285.50 Matches: 62
Percent Similarity: 56.97% Conservative: 32
Best Local Similarity: 37.58% Mismatches: 58
Query Match: 11.17% Indels: 13
DB: 7 Gaps: 4

US-10-813-588-2 (1-487) x US-11-128-061-3655 (1-1400)
Qy 201 AaNGlyCySeSerArgSerLeuSerPheGlu-----ProAspGlyGlnIleArg 216
|||
Db 915 AATAGTTGCAGCATGCCATTGGGAATGGAGATAAGCAATATCAGATGCACAGATTACT 974
|||||

Qy 217 AlaSerSerSerTrpGlnSerValAanGluSerGlyAspGlnValHisTrpSerProGly 236
|||||
Db 975 GCTTCATCTCTACTTTACCAATATGTTGCCACC-----TGGTCTCTCTCA 1019
|||||

Qy 237 GlnAlaArgLeuGlnAaspGlnGlyProSerTrpAlaSerGlyAspSerAanAanHis 256
|||||
Db 1020 AAAGCTCGACTTCACCTCCAGGAGGAGGATGCTCGGAGACCTCAGGTGAATAT- 1076
|||||

Qy 257 LysProArgGluTrpLeuGluIleAaspLeuGlyLysLysLysIleThrGlyIleArg 276
|||||
Db 1077 ---CCAAAAGAGTGGCTGCAAGTGGACTTCCAGAGACAATGAAGATCAGCAGGTAAC 1133
|||||

Qy 277 ThrThrGlySerThrGlnSerAanPheAanPheThrValIysSerPheValMetAanPhe 296
|||||
Db 1134 ACTCAGGAGTAAATCTCTGCTTACCAGCATGTATGTGAAGGAGTCTCTCATCTCCAGC 1193
|||||

Qy 297 LysAanAanAanSerLysTrpLysThrLysGlyIleValAanAanGluGluLysVal 316
|||||
Db 1194 AGTCAAGATGGCATCAGTGGACTCTCTTT-----TTTCAGATGCGCAAGTAAGTT 1247
|||||

Qy 317 PheGlnGlyAanSerAanPheArgAspProValGlnAanAanPheIleProIleVal 336
|||||
Db 1248 TTTTCAGGGAATCAAGACTCTCTTACACCTGTGTGTAATCTCTCTAGACCCACCGTTACTG 1307
|||||

Qy 337 AlaArgTyrValArgValProGlnThrTrpHisGlnArgIleAlaLeuLysValGlu 356
|||||
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Db 1308 ACTGCTACCTTCGAATTCACCCCGAGAGTTGGGTGCACAGATTGCCCTGAGGATGGAG 1367
Qy 357 LeuIleGlyCySeGln 361
|||||
Db 1368 GTTCTGGGCTGGAG 1382
|||||

RESULT 5
US-11-128-061-13
; Sequence 13, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 4374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-128-061-13

Alignment Scores:
Pred. No.: 3e-20 Length: 4374
Score: 285.50 Matches: 62
Percent Similarity: 56.97% Conservative: 32
Best Local Similarity: 37.58% Mismatches: 58
Query Match: 11.17% Indels: 13
DB: 7 Gaps: 4

US-10-813-588-2 (1-487) x US-11-128-061-13 (1-4374)
Qy 201 AaNGlyCySeSerArgSerLeuSerPheGlu-----ProAspGlyGlnIleArg 216
|||
Db 3889 AATAGTTGCAGCATGCCATTGGGAATGGAGATAAGCAATATCAGATGCACAGATTACT 3948
|||||

Qy 217 AlaSerSerSerTrpGlnSerValAanGluSerGlyAspGlnValHisTrpSerProGly 236
|||||
Db 3949 GCTTCATCTCTACTTTACCAATATGTTGCCACC-----TGGTCTCTCTCA 3993
|||||

Qy 237 GlnAlaArgLeuGlnAaspGlnGlyProSerTrpAlaSerGlyAspSerAanAanHis 256
|||||
Db 3994 AAAGCTCGACTTCACCTCCAGGAGGAGGATGCTCGGAGACCTCAGGTGAATAT- 4050
|||||

Qy 257 LysProArgGluTrpLeuGluIleAaspLeuGlyLysLysLysIleThrGlyIleArg 276
|||||
Db 4051 ---CCAAAAGAGTGGCTGCAAGTGGACTTCCAGAGACAATGAAGATCAGCAGGTAAC 4107
|||||

Qy 277 ThrThrGlySerThrGlnSerAanPheAanPheThrValIysSerPheValMetAanPhe 296
|||||
Db 4108 ACTCAGGAGTAAATCTCTGCTTACCAGCATGTATGTGAAGGAGTCTCTCATCTCCAGC 4167
|||||

Qy 297 LysAanAanAanSerLysTrpLysThrLysGlyIleValAanAanGluGluLysVal 316
|||||
Db 4168 AGTCAAGATGGCATCAGTGGACTCTCTTT-----TTTCAGATGCGCAAGTAAGTT 4221
|||||

Qy 317 PheGlnGlyAanSerAanPheArgAspProValGlnAanAanPheIleProIleVal 336
|||||
Db 4222 TTTTCAGGGAATCAAGACTCTCTTACACCTGTGTGTAATCTCTCTAGACCCACCGTTACTG 4281
|||||

Qy 337 AlaArgTyrValArgValProGlnThrTrpHisGlnArgIleAlaLeuLysValGlu 356
|||||
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Db 4282 ACTCGTACCTTCCGAATTCACCCCGAGTTGGTGCACAGATTCGCTCAGGATGGAG 4341
Qy 357 LeulleGlyCysGln 361
Db 4342 GTTCTGGGCTGCGAG 4356

RESULT 6

US-10-632-645-14
; Sequence 14, Application US/10632645
; Publication No. US20050276787A1
; GENERAL INFORMATION:
; APPLICANT: Couto, Linda B.
; APPLICANT: Colosi, Peter C.
; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
; TITLE OF INVENTION: by Target Cells
; FILE REFERENCE: Avigen-04082
; CURRENT APPLICATION NUMBER: US/10/632,645
; PRIOR FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-12-22
; PRIOR FILING DATE: 1999-03-24
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 4999
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-632-645-14

Alignment Scores:
Pred. No.: 3,7e-20 Length: 4999
Score: 285.50 Matches: 62
Percent Similarity: 56.97% Conservative: 32
Best Local Similarity: 37.58% Mismatches: 58
Query Match: 11.17% Indels: 13
DB: 6 Gaps: 4

US-10-813-588-2 (1-487) x US-10-632-645-14 (1-4999)

Qy 201 AnGlyCysSerArgSerLeuSerPheGlu-----ProAspGlyGlnIleArg 216
Db 4304 AATAGTTGAGCATGTCATTTGGGAATGGAGAGTAAGCAATATCATGATGCACAGATTACT 4363
Qy 217 AlaSerSerSerTrpGlnSerValaenGluSerGlyAspGlnValHisTrpSerProGly 236
Db 4364 GCTTCATCTACTTTTACCACATATGTTGCCAC-----TGGTCTCTCTCA 4408
Qy 237 GlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHis 256
Db 4409 AAAGCTCGACTTCACCTCCAGGGAGGAGTAAATGCTGGAGACCTCAGGTGAATAAT--- 4465
Qy 257 LysProArgGluTrpLeuGluLeuLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 276
Db 4466 ---CCAAAAGAGTGGTGCAGTGGACTTCCAGAGACAAATGAAAGTCAAGAGTAATACT 4522
Qy 277 ThrThrGlySerThrGlnSerAsnPheAsnPheValLysSerPheValMetAsnPhe 296
Db 4523 ACTCAGGGAGTAAATCTCTGCTTACCAGCATGATGTAAGAGAGTCTCTCATCTCCAGC 4582
Qy 297 LysAsnAsnAsnSerLysTrpLysThrTrpLysGlyIleValAsnAsnGluGlyVal 316
Db 4583 AGTCAAGATGGCCATCAGTGGACTCTCTTT-----TTTCAGATGGCAAGTAAGGTT 4636
Qy 317 PheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPheIleProProIleVal 336
Db 4636 AGTCAAGATGGCCATCAGTGGACTCTCTTT-----TTTCAGATGGCAAGTAAGGTT 4636

Db 4637 TTTTCAGGGAAATCAAGACTCTCTTACACCTGTGGTGAACCTCTCTAGACCCACCGTTACTG 4696
Qy 337 AlaArgTrpValArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGlu 356
Db 4697 ACTCGCTACCTTCCGAATTCACCCCGAGTTGGTGCACAGATTCGCTCAGGATGGAG 4756
Qy 357 LeulleGlyCysGln 361
Db 4757 GTTCTGGGCTGCGAG 4771

RESULT 7

US-10-632-645-13
; Sequence 13, Application US/10632645
; Publication No. US20050276787A1
; GENERAL INFORMATION:
; APPLICANT: Couto, Linda B.
; APPLICANT: Colosi, Peter C.
; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
; TITLE OF INVENTION: by Target Cells
; FILE REFERENCE: Avigen-04082
; CURRENT APPLICATION NUMBER: US/10/632,645
; PRIOR FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-12-22
; PRIOR FILING DATE: 1999-03-24
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11933
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-632-645-13

Alignment Scores:
Pred. No.: 1.45e-19 Length: 11933
Score: 285.50 Matches: 62
Percent Similarity: 56.97% Conservative: 32
Best Local Similarity: 37.58% Mismatches: 58
Query Match: 11.17% Indels: 13
DB: 6 Gaps: 4

US-10-813-588-2 (1-487) x US-10-632-645-13 (1-11933)

Qy 201 AnGlyCysSerArgSerLeuSerPheGlu-----ProAspGlyGlnIleArg 216
Db 4279 AATAGTTGAGCATGTCATTTGGGAATGGAGAGTAAGCAATATCATGATGCACAGATTACT 4338
Qy 217 AlaSerSerSerTrpGlnSerValaenGluSerGlyAspGlnValHisTrpSerProGly 236
Db 4339 GCTTCATCTACTTTTACCACATATGTTGCCAC-----TGGTCTCTCTCA 4383
Qy 237 GlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHis 256
Db 4384 AAAGCTCGACTTCACCTCCAGGGAGGAGTAAATGCTGGAGACCTCAGGTGAATAAT--- 4440
Qy 257 LysProArgGluTrpLeuGluLeuLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 276
Db 4441 ---CCAAAAGAGTGGTGCAGTGGACTTCCAGAGACAAATGAAAGTCAAGAGTAATACT 4497
Qy 277 ThrThrGlySerThrGlnSerAsnPheAsnPheValLysSerPheValMetAsnPhe 296
Db 4498 ACTCAGGGAGTAAATCTCTGCTTACCAGCATGATGTAAGAGAGTCTCTCATCTCCAGC 4557
Qy 297 LysAsnAsnAsnSerLysTrpLysThrTrpLysGlyIleValAsnAsnGluGlyVal 316
Db 4558 AGTCAAGATGGCCATCAGTGGACTCTCTTT-----TTTCAGATGGCAAGTAAGGTT 4611

QY 317 PheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPheIleProProfilLeVal 336
Db 4612 TTTACGGGAAATCAAGACTCTTCCACACTGTGGTGAATCTCTAGACCCACCGTTACTG 4671
QY 337 AlaArgTyrValArgValProGlnThrTrpHisGlnArgIleAlaLeuLysValGlu 356
Db 4672 ACTCGCTACTCTCGAATTCACCCAGAGTTGGTGCCACAGATTGCCCTGAGGATGGAG 4731
QY 357 LeuIleGlyCysGln 361
Db 4732 GTTCTGGCTGCGAG 4746

RESULT 8

US-11-136-527-989/c
; Sequence 989, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 989
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-989

Alignment Scores:
Pred. No.: 3.5e-21 Length: 452
Score: 280.00 Matches: 54
Percent Similarity: 63.36% Conservative: 29
Best Local Similarity: 41.22% Mismatches: 46
Query Match: 10.95% Indels: 2
DB: 7 Gaps: 1

US-10-813-588-2 (1-487) x US-11-136-527-989 (1-452)

QY 232 HistTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAep 251
Db 425 TACTGGGAGCCTTCCCTTGGCCGCTGAATGCCAGGCCGAGTGAATGCTTGGCAAGCC 366
QY 252 SerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyLysLys 271
Db 365 AAGGCAACAACAACAG-----CAGTGGTTACAATTTGATCTGCTCAAAATCAAGAAG 312
QY 272 IleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLysSer 291
Db 311 GTAACGGCCATCGTAACCTCAGGTTGCAAGTCTCTGCTCTGAGATGATGTGAAGAGC 252
QY 292 PheValMetAsnPheLysAsnAsnAsnSerLysTrpLysThrTyrLysGlyIleValAsn 311
Db 251 TACAGCATCTCTGTCAGTGACCGGGGTCTCTCTGGAAACCCCTACCGGAGAAATCTCTCC 192
QY 312 AsnGluGlyLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPhe 331
Db 191 ATGGTGACAAGATTTTGAAGGGAATAGCAATACCAAGGGCATATGAAGAATCTTTTC 132
QY 332 IleProProIleValAlaArgTyrValArgValProGlnThrTrpHisGlnArgIle 351
Db 131 AACCCACTATTATTTCAGATTTATCCGAATTCCTTAACCTGGAACCAAGTATT 72
QY 352 AlaLeuLysValGluLeuIleGlyCysGlnIle 362
Db 71 GCACCTTCGCTGGAACCTCTTCGGCTGTGACATT 39

RESULT 9

US-11-136-527-5085
; Sequence 5085, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5085
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5085

Alignment Scores:
Pred. No.: 3.5e-21 Length: 452
Score: 280.00 Matches: 54
Percent Similarity: 63.36% Conservative: 29
Best Local Similarity: 41.22% Mismatches: 46
Query Match: 10.95% Indels: 2
DB: 7 Gaps: 1

US-10-813-588-2 (1-487) x US-11-136-527-5085 (1-452)

QY 232 HistTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAep 251
Db 28 TACTGGGAGCCTTCCCTTGGCCGCTGAATGCCAGGCCGAGTGAATGCTTGGCAAGCC 87
QY 252 SerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyLysLys 271
Db 88 AAGGCAACAACAACAG-----CAGTGGTTACAATTTGATCTGCTCAAAATCAAGAAG 141
QY 272 IleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLysSer 291
Db 142 GTAACGGCCATCGTAACCTCAGGTTGCAAGTCTCTGCTCTGAGATGATGTGAAGAGC 201
QY 292 PheValMetAsnPheLysAsnAsnAsnSerLysTrpLysThrTyrLysGlyIleValAsn 311
Db 202 TACAGCATCTCTGTCAGTGACCGGGGTCTCTCTGGAAACCCCTACCGGAGAAATCTCTCC 261
QY 312 AsnGluGlyLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPhe 331
Db 262 ATGGTGACAAGATTTTGAAGGGAATAGCAATACCAAGGGCATATGAAGAATCTTTTC 321
QY 332 IleProProIleValAlaArgTyrValArgValProGlnThrTrpHisGlnArgIle 351
Db 322 AACCCACTATTATTTCAGATTTATCCGAATTCCTTAACCTGGAACCAAGTATT 381
QY 352 AlaLeuLysValGluLeuIleGlyCysGlnIle 362
Db 382 GCACCTTCGCTGGAACCTCTTCGGCTGTGACATT 414

RESULT 10

US-10-947-249-162
; Sequence 162, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: Akira NAKAGAWARA
; APPLICANT: Miki OHIRA
; APPLICANT: Shin ISHII
; APPLICANT: Takeshi GOTO
; APPLICANT: Hiroyuki KUBO
; APPLICANT: Takahiro HIRATA
; APPLICANT: Yasuko YOSHIDA
; APPLICANT: Saichi YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Met

```
FILE REFERENCE: 117007
CURRENT APPLICATION NUMBER: US/10/947,249
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/505,614
PRIOR APPLICATION NUMBER: 2003-09-25
NUMBER OF SEQ ID NOS: 200
SOFTWARE: PatentIn version 3.1
SEQ ID NO 162
LENGTH: 3935
TYPE: DNA
ORGANISM: Homo sapiens
US-10-947-249-162

Alignment Scores:
Pred. No.: 1,13e-12 Length: 3935
Score: 217.00 Matches: 55
Percent Similarity: 44.39% Conservatives: 40
Best Local Similarity: 25.70% Mismatches: 97
Query Match: 8.49% Indels: 22
DB: 6 Gaps: 5

US-10-813-588-2 (1-487) x US-10-947-249-162 (1-3935)
QY 212 AspGlyGlnIleArgAlaSerSerTrpGln---SerValAsnGluSerGlyAspGln 230
DB 1328 GACAACACAGATCCAGACCTCTCCATGCTGGCCACCGCTGGGGGCACAGCGCGCGG 1387
QY 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
DB 1388 CTCACACATGACACCGGCTCCACTGAGGACGACTACTATGATGGTGGTGGTGGCAG 1447
QY 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLysLys 270
DB 1448 GACGATGCCAGGACC-----CAGTGGATAGAGTGGACACACAGGAGGACTACC 1495
QY 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTrpValLys 290
DB 1496 CGGTTTCACAGCGGTCTATCACCAGGCGCAGAGACTCCAGCATCCATGACGATTTGTGACC 1555
QY 291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrTrpLysGlyIleVal 310
DB 1556 ACCTTCTTCGTGGGCTTCAGCAATGATGACACGACATGGGTGATGTACACCAAC----- 1609
QY 311 AsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
DB 1610 GCCTATGAGGAATGACCTTTCATGGACAGTGGACAGGACACACCCGCTGTGAGTGAG 1669
QY 331 PheIleProProIleValAlaArgTyrValArgValProGlnThrTrpHisGlnArg 350
DB 1670 CTCACAGAGCGGTGGTGGTCTGTTTCATCCGATCTACCCACTCACCCTGGAATGGCAGC 1729
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGln----- 364
DB 1730 CTGTGATCGGCTGGAGTGTGGGGTCTCTGTGGCCCTCTCTACAGCTACTACGCA 1789
QY 365 -----GlyAsnAspSerLeuValTrpArg-----LysThrSer 375
DB 1790 CAGATAGGTGGTGGCCACCATGACCTGGATTTCGGACACACAGCTACAGGACATG 1849
QY 376 GlnSerThrSerValSerThrLysLysGluAspGluThrIleThrArgProIleProSer 395
DB 1850 CGCCAGCTCATGAAGGTGGTGAACAGGAGTGTCCCAACCATCAGCCGCACTTACAGCCTG 1909
QY 396 GluGluThrSerThrGlyIleAsnIleThrThrValAlaIle 409
DB 1910 GGCAAGAGCTACGAGGCGCTCAAGATCTATGCCATGGAGATC 1951

RESULT 11
US-10-131-826A-391
; Sequence 391, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 391
LENGTH: 3772
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-391

Alignment Scores:
Pred. No.: 4.47e-09 Length: 3772
Score: 184.50 Matches: 72
Percent Similarity: 42.81% Conservatives: 47
Best Local Similarity: 25.90% Mismatches: 105
Query Match: 7.22% Indels: 55
DB: 6 Gaps: 12

US-10-813-588-2 (1-487) x US-10-131-826A-391 (1-3772)
QY 130 AlaGlyAspIleSerGlyAsnMetVal-----AspGlyTyrArgAspThrSerLeu 146
DB 436 GCAGGAGATCTGGAGCCCGGAGCCCTACTACTACGCGCGCCGAGCCGAGCTCGAGACCTT 495
QY 147 LeuCysLysAlaAlaIleHisAla-----GlyIleIleAlaAspGluLeuGlyGln 164
DB 496 CTCCTCCGCGCTGCTGGCGGCGCGGAGAGTGGGAGCGCGCCCGCCAGGAGCCAG 555
QY 165 IleSerValLeuGlnArgLysGly-----IleSerArgTyrGluGlyIleLeu 180
DB 556 GCCGCC-----CAAGAGGCCACCCAGCCCAAGAGAGTCTCCAGAGGAGGAGATC 606
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerArgAspGlySerLeuPheThrSer 200
```

Db 607 GGCTCGGAGCGCCCTCCA--CCAGGTAAACACAGCAACAAAAAGTTATGAAACCAAG 664
QY 201 AenGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
Db 665 -----AGCTCTGAGAAGGCTGCCAACGATGATCACAGTGTCTGGTGGCCCGT--- 712
QY 221 TrpGlnSerValAsnGluSer-----Gly 228
Db 713 --GAAGATGTCAGAGAGAGTTGCCACCTCTTGGTCTGGAAACCTTAAATAATCACAGAC 769
QY 229 AspGlnValHisTrpSer-----ProGlyGlnAlaArgLeu 240
Db 770 TTCACGCTCATGCTCCACGGTGAAGCGCTATGGCTGGGGGCACATCAGGGGACATC 829
QY 241 GlnAspGlnGly-----ProSerTrpAlaSerGlyAsp 251
Db 830 AACATCCAGCGGGCCATTAAATGAATGATTTTATGACGGAGCGTGGTGGCGGGA--- 886
QY 252 SerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGlnLysLys 271
Db 887 -----AGAAATGACCTCCACGACAGTGTGAAGTGAAGTGGATGCTCGGCGCTGACACAGA 937
QY 272 IleThrGlyIleArgThrGlySerThrGlnSerAsnPheAsnPheTyrValLysSer 291
Db 938 TTCACGTGGTGTATCACTCAAGGGAGGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCC 997
QY 292 PheValMetAsnPheLysAsnAsnSerLysTrpLysTrpLysGlyIleValAsn 311
Db 998 TATAAGGTCACTGGTGACATGACACCCACCTGGTCACTGTTAAGAAAT-----GGA 1051
QY 312 AsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPhe 331
Db 1052 TCTGGAGCATGATATTTAGGGGAAACAGTGAAGAGGAGATCCCTGTCTCAATGAGCTA 1111
QY 332 IleProProIleValAlaArgTyrValArgValValProGlnThrTrpHisGlnArg--- 350
Db 1112 CCGTCCCATGGTGGCCCTACATCCGATAAACCTCGATGCTGCTGGTGGTATGATGGG 1171
QY 351 ---IleAlaLeuLysValGluIleGlyCysGlnIleThrGlnGlyAsnAsp 367
Db 1172 AGCATCTGCATGAGATGGAGATCCTGGGCTGCCCATGCCAGCATCTTAATAAT 1225

RESULT 12

US-11-137-465-32
; Sequence 32, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safie, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabanick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-137-465-32

Alignment Scores:
Pred. No.: 2,866-08 Length: 2205
Score: 174.00 Matches: 64
Percent Similarity: 42.86% Conservative: 32
Best Local Similarity: 28.57% Mismatches: 84
Query Match: 6.80% Indels: 47
DB: 7 Gaps: 5

US-10-813-588-2 (1-487) x US-11-137-465-32 (1-2205)

QY 212 AspGlyGlnIleArgAlaSerSerSerTrp----- 221
Db 379 GATAGCGGCTTGGAGCATCCAGCAGCCAGTCTTTGGTCTTGGACCACACCGAGACCG 438
QY 222 -----GlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAla 238
Db 439 CTCACATTCATCAGGCTCGAGGAGCGCGATCT-ATATGATGGAG-CTTGGTGTGCTG 496
QY 239 ArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysPro 258
Db 497 AGGAG-CAGGACGCCGATCCA----- 516
QY 259 ArgGluTrpLeuGluIleAspLeuGlyGlnLysLysLysIleThrGlyIleArgThr 278
Db 517 -----TGGTTTCAGGTGGACCTGGGCAACCCACCTCTCTCGGGTGTATCACACAG 570
QY 279 GlySerThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsn 298
Db 571 GCGAGAACTCTGTCTGGAGGTATGACTGGGTACATCATACAGGTCCAGTTCAGCAAT 630
QY 299 AsnAsnSerLysTrpLysTrpLysGlyIleValAsnAsnGluGluLysValPheGln 318
Db 631 GACAGTCGACCTGGTGGGGAAGTAGAACACACAGCAGTGGATGGACGCAATTTCTCT 690
QY 319 GlyAsnSerAsnPheArgAspProValGlnAsnAsnPheIleProIleValAlaArg 338
Db 691 GCAATTCAGACCCAGAAATCCAGTGTGAACCTCTCCCGGAGCCCGAGTGGCCCGC 750
QY 339 TyrValArgValValProGlnThrTrpHisGlnArgIleAla-----LeuLysValGlu 356
Db 751 TTCATTGCTGTGCTGCCACGACCTGGCTCCAGGAGCGCGCTTGGCTCCGGGCGAG 810
QY 357 LeuIleGlyCysGlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGln 376
Db 811 ATCTGGCTGCCAGTCTCAGACCCCAATGACCTATTCTTGAGGCCCTGCGTGGGA 870
QY 377 SerThr-SerValSerThrLysLysGluAspGluThrIleThrArgPro----- 392
Db 871 TCCTCTGACCTCTAGACT-----TTCAGCATCAATATACAGGCCCATGAGGAAGCTG 924
QY 393 -----IleProSerGluGluThrSerThrGlyIleAsnIleTh 405
Db 925 ATGAACGAGGTACAGACGAATGCCCCCAACATCACCCTGATCTACAGCATTTGGGAAGC 984
QY 405 rThrValAla 408
Db 985 TACCAGGGCC 994

RESULT 13

US-10-852-893-1
; Sequence 1, Application US/10652893
; Publication No. US2005024973A1
; GENERAL INFORMATION:
; APPLICANT: Balasubramanian, Sriram
; APPLICANT: Ford, John
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MAMMALIAN PROTEASES; RELATED REAGENTS
; FILE REFERENCE: DX0613B
; CURRENT APPLICATION NUMBER: US/10/652,893
; CURRENT FILING DATE: 2003-08-29

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; PRIOR APPLICATION NUMBER: US/09/650,284B
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 08/706,216
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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Alignment Scores:	
Pred. No.:	3,98e-08
Score:	174.00
Percent Similarity:	42.86%
Best Local Similarity:	28.57%
Query Match:	6.80%
DB:	6
Length:	2719
Matches:	64
Conservative:	32
Mismatches:	84
Indels:	47
Gaps:	5

US-10-813-588-2 (1-487) x US-10-652-893-1 (1-2719)

212	Qy	AspGlyGlnIleArgAlaSerSerTrp-----	221
		: : : : :	
715	Db	GATAGCGGGTTCAGGCGATCCAGCAGCCAGTCTTTGGTCTTGGACCACACCGAGGACGG	774
222	Qy	-----GlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAla	238
		: : : : :	
775	Db	CTCAACATTTCAGTCAGGCGCTGGAGGACGGGGATCT-ATATGATGGAG-CCTGGTGTGCTG	832
239	Qy	ArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysPro	258
		: : : : :	
833	Db	AGAG-CAGAGCGCCGATCCA-----	852
259	Qy	ArgGluTrpLeuGluIleAspLeuGlyLysLysLysIleThrGlyIleArgThrThr	278
		: : : : :	
853	Db	-----TGGTTTCAGGTGGAGCTGGGCCCCCAGCGCTTCTCGGGTGTATCACACAG	906
279	Qy	GlySerThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsn	298
		: : : : :	
907	Db	GGCAGGAACCTCTCTCGAGGTATGACTGGGTACATCATACAAGGTCCAGTTCAGCAAT	966
299	Qy	AsnAsnSerLysIleTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGln	318
		: : : : :	
967	Db	GACAGTCGGACCTGGTGGGAAGTAGGACCAACAGCAGTGGGATGGACGAGTATTCCT	1026
319	Qy	GlyAsnSerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArg	338
		: : : : :	
1027	Db	GCCAAATCAGACCAGNAACCTCAGTGCTGAACTCTCTGCGGAGCCCCCAGGTGGCCCGC	1086
339	Qy	TyrValArgValValProGlnThrTrpHisGlnArgIleAla-----LeuLysValGlu	356
		: : : : :	
1087	Db	TTCAATTCGCTGTGCCCCAGACTGGCTCCAGGAGCGCGCTTGCCTCCGGGCGAG	1146
357	Qy	LeuIleGlyCysGlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGln	376
		: : : : :	
1147	Db	ATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCTTGAGGCCCCGTGGCGGA	1206
377	Qy	SerThr-SerValSerThrLysLysGluAspGluThrIleThrArgPro-----	392
		: : : : :	
1207	Db	TCCTCTGACCCCTCTAGACT-----TTCAGCATCAAAATTACAGGCCATATGAGAAGCTG	1260
393	Qy	-----IleProSerGluGluThrSerThrGlyIleAsnIleThr	405
		: : : : :	
1261	Db	ATGAGCAGGTACAGAGCAATCCCCCAACATCACCCGCATCTACAGCATTGGGAAGAC	1320
405	Qy	rThrValAla	408
1321	Db	TACGAGGGCC	1330

RESULT 14

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US-11-150-883-49
; Sequence 49, Application US/11150883
; Publication No. US2006002937A1
; GENERAL INFORMATION:
; APPLICANT: Schwabe, H.W.
; APPLICANT: Stover, C.M.
; APPLICANT: Tedford, C. E.
; APPLICANT: Parent, J.B..
; APPLICANT: Fujita, T.
; TITLE OF INVENTION: METHODS FOR TREATING C
; TITLE OF INVENTION: COMPLEMENT ACTIVATION
; FILE REFERENCE: OMER-1-25400
; CURRENT APPLICATION NUMBER: US/11/150,883
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/578,847
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 4960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-150-883-49

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Alignment Scores:	
Pred. No.:	3.25e-07
Score:	169.50
Percent Similarity:	42.56%
Best Local Similarity:	23.08%
Query Match:	6.63%
DB:	7
Length:	4960
Matches:	66
Conservative:	56
Mismatches:	126
Indels:	39
Gaps:	11

US-10-813-588-2 (1-487) X US-11-150-883-49 (1-4960)

[illegible]

```

Db      3635 CTACCCAGTGGCGAGTGGAGTACATCACAGGTCCTGGAGTGCACCACTACAAAGCTGTG 3694
QY      180 LeuAlaAsnGlyValLeuSerArg-----AspGlySerLeuSerAspLysArgPheLeu 197
Db      3695 ATTCACTACAGCTGTGAAGAGACCTTCTACACATGAAGTGAATGATGGTAAATATGTG 3754
QY      198 PheThrSerAsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAla 217
Db      3755 TGTGAGGCTGATGATCTCGACGAGCTCCAAAGGAGAAATCACTCCAGTCTCTGTGAG 3814
QY      218 SerSerSerTrpGlnSerValaGlnSerGlyValHisTrpSerProGlyGln 237
Db      3815 CCTGTTTGTGCACTATCAGCCGCCACCAACAGGAGCGGTATATA-TGG----- 3861
QY      238 AlaArgLeuGlnAspGlnGlyProSerTrp-----AlaSerGlyAspSerSer 253
Db      3862 -----AGGCCAAAGGCAAAACCTGTGTGATTTCTTGTGGCAAGTCTGTATATTAGG 3912
QY      254 AsnAsnHisLysProArg 259
Db      3913 TGGAAACACACAGCAGCAGG 3930

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RESULT 15

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US-11-128-061-787
; Sequence 787, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 787
; LENGTH: 2521
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (642)..(676)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1092)..(1113)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-787

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Alignment Scores:
Fred. No.: 1.28e-07 Length: 2521
Score: 169.00 Matches: 54
Percent Similarity: 49.40% Conservative: 28
Best Local Similarity: 32.53% Mismatches: 60
Query Match: 6.61% Indels: 25
DB: 7 Gaps: 8

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US-10-813-588-2 (1-487) x US-11-128-061-787 (1-2521)

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QY      211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValaGlnSerGlyAspGln 230
Db      109 CCAGATGAGCAGCATACAGCTTCAAGTCAGTGTGTGAGCA-ATCCAC-----GGCTGCCAG 161

```

```

QY      231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAla----- 248
Db      162 ATA---TGGAGGCTGGACTCTGAAGAAGGAGA-----TGGAGCCTGGTG 203
QY      249 SerGlyAspSerSerAsnAsnHisLysPro-ArgGluTrpLeuGluIleAspLeuGlyG1 268
Db      204 TCCGAGATTCCAGTGCACACCCGATGACCTGGAAGAAATTTCTGCAGATTGACTTACGTAC 263
QY      268 uLysLysLysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPhe-- 287
Db      264 CCTCCACTTTATCACTCTTGTGGGAGCCCGAGGACGTCATGCGGGGGGTCATGGCATTGA 323
QY      288 -TyrValLysSerPheValMetAsnPhelysAsnAsnSerLysTrpLysThrTrpLys 307
Db      324 ATATGCACCATGTATCAAGATCAACTATAGTCGAGATGGCACTCGCTGGATCTCTGGGG 383
QY      307 sGlyIleValAsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspProVa 327
Db      384 TAAT-----CGCATGGAAAGCAGGTGTAGATGGGAACAGTAACCTTATGATGCTTT 437
QY      327 lGlnAsnAsnPheIleProIleValAlaArgTyrValArgValValProGlnThrTr 347
Db      438 CCTGAAGGACCTGGAGCCACCCATTGTAGCCAGATTGTTCGCTTATCCAGTCACTGA 497
QY      347 PHis---GlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGlnGlyAs 366
Db      498 CCACTCCATGAATGTGTGATGAGGGTTGAGCTTTATGTTGT----- 540
QY      366 nAspSerLeuValTyr 371
Db      541 -----GTCTGG 546

```

Search completed: January 15, 2006, 23:30:12
Job time : 412 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:27:38 ; Search time 4505 Seconds
(without alignments)
5057.782 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNYPGTYPNHTVCEKTI.....YDNEKEVTKQLDITSDMAG 487

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-O=/cpn2.1/USPTO.spool_p/US10813588/runat_12012006_171131_15401/app.query.fasta_1.647
-DB=EST-QPWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10813588 @CGN 1.1 8010 @runat_12012006_171131_15401 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hgc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss2:*
10: gb_gss2:*
11: gb_gss3:*

CR749448 3600 bp mRNA linear HTC 19-AUG-2004
LOCUS Homo sapiens mRNA; cDNA DKFZp686L21135 (from clone DKFZp686L21135).
DEFINITION CR749448
ACCESSION CR749448
VERSION CR749448.1 GI:51476605
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 3600)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

REFERENCE

AUTHORS

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2036	79.6	3600	CR749448	
2	1512.5	59.2	1031	3 BM558496	CR749448 Homo sapi
3	1289.5	50.4	839	6 CF785931	BM558496 AGENCOURT
4	1180.5	46.2	961	5 BUI77739	CF785931 AGENCOURT
5	1155.5	45.2	1924	4 AK016485	BUI77739 AGENCOURT
6	1154.5	45.2	2835	4 AK014521	AK016485 Mus muscu
7	1154	45.1	652	7 CN404610	AK014521 Mus muscu

8	1014.5	39.7	866	8 DNI34443	DNI34443 999656 MA
9	896	35.0	956	5 BY713935	BY713935 BY713935
10	879.5	34.4	913	6 CD109068	CD109068 AGENCOURT
11	861	33.7	865	8 CX498307	CX498307 JGI_XZG44
12	850	33.2	770	6 CB988462	CB988462 AGENCOURT
13	820	32.1	864	8 DR845229	DR845229 JGI_CABEL
14	802	31.4	830	7 CN440576	CN440576 BE0402281
15	795.5	31.1	872	2 BG245910	BG245910 602358725
16	769	30.1	736	8 CX755002	CX755002 AGENCOURT
17	765	29.9	683	5 BX360287	BX360287 BX360287
18	762	29.8	805	8 CX417452	CX417452 JGI_XZG64
19	756	29.6	686	5 BX345014	BX345014 BX345014
20	756	29.6	745	5 BU449584	BU449584 603217463
21	747.5	29.2	883	2 BG975603	BG975603 602845306
22	729.5	28.5	935	6 CA986706	CA986706 AGENCOURT
23	727	28.4	466	1 AW390343	AW390343 RC4-ST018
24	721	28.2	798	6 CB960471	CB960471 AGENCOURT
25	707.5	27.7	4121	4 AK051889	AK051889 Mus muscu
26	695.5	27.2	860	3 BJ728454	BJ728454 BJ728454
27	673	26.3	478	10 CG521977	CG521977 OST90814
28	661	25.9	434	1 AW483656	AW483656 55586 MAR
29	650	25.4	425	10 C2293584	C2293584 P077F07 G
30	646	25.3	1150	3 BM805721	BM805721 AGENCOURT
31	643	25.1	790	6 CB959630	CB959630 AGENCOURT
32	642.5	25.1	899	6 CA791785	CA791785 AGENCOURT
33	636.5	24.9	802	6 CD110061	CD110061 AGENCOURT
34	625	24.4	404	11 DQ039380	DQ039380 Homo sapi
35	625	24.4	404	11 DQ039381	DQ039381 Pan trogl
36	625	24.4	409	10 C2293317	C2293317 P076F06 G
37	625	24.4	600	5 BU924048	BU924048 7074-50 M
38	624	24.4	462	10 CL639277	CL639277 G085B03 G
39	623	24.4	417	10 C2293527	C2293527 P075B07 G
40	619	24.2	426	10 C2293590	C2293590 P077E08 G
41	614	24.0	402	10 C2293313	C2293313 P076F07 G
42	609	23.8	348	7 CN404612	CN404612 170005999
43	585	22.9	911	8 DN063593	DN063593 JGI_CABDI
44	582	22.8	857	8 CX889725	CX889725 JGI_CANM2
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ALIGNMENTS

FEATURES

Location/Qualifiers

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ORIGIN

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Alignment Scores:
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Score: 2036.00 Matches: 461
Percent Similarity: 43.61% Conservative: 0
Best Local Similarity: 43.61% Mismatches: 2
Query Match: 79.62% Indels: 596
DB: 4 Gaps: 3

US-10-813-588-2 (1-487) x CR749448 (1-3600)

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Db 253 ATGACATCTAAGAAATATATCCCGGAGCTACCCCAATCACACTGTTTGCAGAAAGACAAAT 312

Qy 21 ThrValProIysGlyIysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db 313 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTGGATATCGAATCCAG 372

Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 373 ACCTGTGCTCTCACTACTCTCTTCCACAGCTCTTCAGATCAATATGTCCTCACTGT 432

Qy 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 433 GGAAGTATGACTGTCTCCAAAGAACTCTTGTGAACAAAGTGAAGTAACCGTCCGCTTT 492

Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 493 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGACCTATGCGAGCAGGACCAT 552

Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerIys 120
Db 553 CCAGATTAAACATGTTTTGGAACGAGCTAGCCATTAATTTGAAGACAGAATACAG --- 608

Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 608 ----- 608

Qy 141 TyrArgAspThrSerLeuLeuCysIysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 609 -----ACCTCTTATTGTGAAGCTGCCATCCATGCGAAGTAATTCGTGATGA 659

Qy 161 LeuGlyGlyGlnIleSerValLeuGlnArgIysGlyIleSerArgTyrGluGlyIleLeu 180
Db 660 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCTG 719

Qy 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspIysArgPheLeuPheThrSer 200
Db 720 GCCATGGTGTCTTTTCGAGGATGGTTCCCTGTGCAGCAAGCGATTCTGTATTACCTCC 779

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Qy 201 AenGlyCysSerArgSerIleuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
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Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnIleArgLeu 240
Db 840 TGGCAGTCGGTCAATGAGAGTGGAGCAAGTTCATCGTCTCTCTGGCCAAAGCCGACTT 899

Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisIysProArgGlu 260
Db 900 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGCAGTAGCAACAACAACACACGAGAG 959

Qy 261 TrpLeuGluIleAspLeuGlyGlyIysIysIleThrGlyIle----- 275
Db 960 TGGCTGGAGATCGATTTGGGGGAGAAAAAAGAAAAATAACAGGTGC-AGAAAAATAACACA 1018

Qy 275 ----- 275

Db 1019 TGCCAAAGTCAGAGTAGTTTCATGCTGTAAATGACTCGCAGTTGAAAAATAGCCTTATT 1078

Qy 275 ----- 275

Db 1079 GTTTACATAGTGCTTCTCTACCTACCTCCAAGTTCTTGAAATATTTGAAATGTAAACA 1138

Qy 275 ----- 275

Db 1139 ATCTTTTACATTCTTTCTGTGAAAAAGAAATCTGTATGCAAGTTGTAAATATATGATAT 1198

Qy 275 ----- 275

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Qy 275 ----- 275

Db 1259 TTAATCTGTGAAGAGATTTTAAATGCAACTAATAATATAGTTGGCTGTGAGATGATCTGA 1318

Qy 275 ----- 275

Db 1319 GGTTTCAAAATGAGGAGAAAAAATGAAACTTGAAATTTATAATAGATGTTTATATTTAAACA 1378

Qy 276 -----ArgThrThrGlySer 280
Db 1379 AACTTTTAAAAATAGCCTGTAAATATATTTCTTACAAGGAATTAGGCCACAGATCT 1438

Qy 281 ThrGlnSerAsnPheAsnPheTyrValIysSerPheValMetAsnPheIysAsnAsn 300
Db 1439 ACACAGTCCGACTTCAACTTTTATGTTAAGAGTTTTTGTGATGAACITTCAAAAACAATAAT 1498

Qy 301 SerLysTrpIysThrTyrIysGlyIleValAsnAsnGluGluIys----- 315
Db 1499 TCTAAGTGAAGACCTTATAAGGAATTTGTAATTAATGAAGAAAAAGGTAAGAGTAACCCCT 1558

Qy 315 ----- 315

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Qy 315 ----- 315

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Qy 315 ----- 315

Db 1679 CCAAGCTTTGGGAAGCCAAGCGAGGAGGATCATTTTGAGACCATCTCTGGGCAACATAGCAA 1738

Qy 315 ----- 315

Db 1739 GACCCCAACCACTACAAAAAATAATTTTAAATACCCAAATGTGGTGTGCACACTTGTAG 1798

Qy 315 ----- 315

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Score:             1512.50           Matches:           312
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Query Match:       59.15%            Indels:          12
DB:                3                Gaps:             2

US-10-813-588-2 (1-487) x BM558496 (1-1031)

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Db 1 CCCAATCACACTGTTTGCAGAAAGACAATACAGTACCAAGGGGAAAGACTGATTCTG 60
QY 31 ArgLeuGlyAspLeuAspIleGluSerGlnThrCysAlaSerAspTyrLeuLeuPheThr 50
Db 61 AGGTTGGGAGATTGGATATCGAATCCAGACCTGTGCTTCTGACTATCTTCTTCCACC 120
QY 51 SerSerSerAspGlnTyrGlyProTyrCysGlySerMetThrValProLysGluLeuLeu 70
Db 121 AGCTCTTCAGATCAATATGTCATATGTCATGTCGGAAGTATGACTGTTCCCAAGAACTCTTG 180
QY 71 LeuAsnThrSerGluValThrValArgPheGluSerGlySerHisIleSerGlyArgGly 90
Db 181 TTGAACACAAGTGAAGTACCGTCCGCTTTGAGATGGATCCACATTTCTGCGCGGGT 240
QY 91 PheLeuLeuThrTyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAla 110
Db 241 TTTTTCGTGACCTATCGAGACGACGACCATCCAGATTTAATAACATGTTTGGAAACGAGCT 300
QY 111 SerHisTyrLeuLeuThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAla 130
Db 301 AGCCATTTATTGAAGACAGAAATACAGCAATTCGCCAGCTGGTTGTAGAGACGTAGCA 360
QY 131 GlyAspIleSerGlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAla 150
Db 361 CGAGACATTTCTGGGAATATGTTAGATGATATAGATACCTCTTTATTGTGCAAGCT 420
QY 151 AlaIleHisAlaGlyIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArg 170
Db 421 GCCATCCATCGCAAGATAATTGCTGATGAACATAGTGGCCAGATCATGTCCTCAGCGC 480
QY 171 LysGlyLysSerArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySer 190
Db 481 AAGGGATCATGTCATGATGAAGGATTTCTGGCAATGGTGTCTTTTCGAGGGATGTTCC 540
QY 191 LeuSerAspLysArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu 210
Db 541 CTGTCAGACAAGCGATTCTCTGTTTACCTCAATGGTTGCAGCAGATCCTTTGAGTTTGA 600
QY 211 ProAspGlyGlnIleArgAlaSerSerSerTyrGlnSerValAsnGluSerGlyAspGln 230
Db 601 CCTGACGGGCAATCAGAGCTTCTTCTCATGTCAGCTCGGTCAATGAGAGTGAGACCAA 660
QY 231 ValHisTyrSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTyrAlaSerGly 250
Db 661 GTTCACCTGGTCTCCTGGCCAAAGCCGACTTCAGAGCCAGCCCATCATGGCTTCGGCC 720
QY 251 AspSerSerAsnHisLysProArgGlu-TyrLeuGluIleAspLeuGlyGlyLys 270
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Db 781 GAAAAATAACAGGGATTAGGACCAAGGATCTACAGATCGAAGATCTTCACTTTTATGNTTA 840
QY 290 YSerPheValMetAsnPheLysAsnAsnSerLysTyrTyrLysGlyLys 310
Db 841 AGAGTTTGTGATGAGATCTCAAAACAT-AATTCTAAGTCGAG-ACCTATAAGGATTC 898
QY 310 aAsnAsnGluGlu--LysValPheGlnGlyAsnSerAsnPheArg-AspProValGln 329
Db 899 TTGATATTGAAGAAAAAGGGGTTACGGGTAACTCTAACTTTTCGGGGACCCATTCGAAA 958
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RESULT 3
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DEFINITION
AGENCY: 15989463 NIH_MGC 220 Homo sapiens cDNA clone
IMAGE: 30707295 5', mRNA sequence.
CF785931
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1071 row: k column: 16
High quality sequence stop: 617.
FEATURES
Location/Qualifiers
1..839
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/note="Organ: mixed; Vector: pYX-Asc; Site 1: EcoRI;
Site 2: NotI; Library is oligo-dT primed and directionally
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gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGGCAGCAGG)3' and 5' (
CCTGTCGCGG)3'. 3' Linker sequence - GCGGCCGTGAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5' d
(AATTAACCTCACTAAGGGA)3'. 5' End: T7 promoter primer 5' d
(TAATACGACTCACTATAGG)3'. Library was constructed in the
laboratory of M. Bento Soares. Average insert size 3-4kb
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
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Best Local Similarity: 92.62% Mismatches: 12
Query Match: 50.43% Indels: 2
DB: 6 Gaps: 2
US-10-813-588-2 (1-487) x CF785931 (1-839)

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 QY 147 LeuCyLeValalaIleHisalaGlyIleIleAlaAspGluLeuGlyGlnIleSer 166
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 QY 167 ValLeuGlnArgLysGlyIleSerArgTyrGlyGlyIleLeuAlaAsnGlyValLeuSer 186
 Db 128 GTGCTTCAGCGCAAGGATCATGATGATGAGGATTCGTGCCAATGGTGTCTTTG 187
 QY 187 ArgAspGlySerLeuSerAspLysArgPheLeuPheThrSerAsnGlyCysSerArgSer 206
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 QY 207 LeuSerPheGluProAspGlyGlnIleArgAlaSerSerSerTrpGlnSerValAsnGlu 226
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 Db 368 TGGGCTTCGGCGACAGTAGACCAACCAACACGAGAGTGGCTGGAGATCGATTG 427
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 Db 788 -----ATCACAGCCCT---CCCTCTCGAGAA 811
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 VERSION BUI77739.1 GI:22691723
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 961)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2348 row: f column: 19

High quality sequence stop: 591.

FEATURES

source

1..961

Location/Qualifiers

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/clone="IMAGE:6106770"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 39"

/note="Organ: pancreas; Vector: pOT87; Site:1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed

by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA

synthesis kit (Stratagene) and Superscript II RT (Life

Technologies)."

ORIGIN

Alignment Scores:

Pred. No.: 9,02e-118 Length: 961
 Score: 1180.50 Matches: 236
 Percent Similarity: 90.77% Conservatives: 10
 Best Local Similarity: 87.08% Mismatches: 14
 Query Match: 46.11% Indels: 11
 DB: 5 Gaps: 3

US-10-813-588-2 (1-487) x BUI77739 (1-961)

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 QY 226 GluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyPro 245
 Db 63 GAGAGTGGAGACCAAGTTCACGTGCTCTCTGCGCAAGCCCGACTTCAGGACCAAGGCCCA 122
 QY 246 SerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAsp 265
 Db 123 TCATCGGCTTCGGCGACAGTAGCAACAACCAACCAACAGAGTGGCTGGAGATCGAT 182
 QY 266 LeuGlyGluLysLysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPhe 285
 Db 183 TTGGGGGAGAAAGAAATAACAGGAATTAGGACCAACAGGATCTACACAGTCGAATTC 242
 QY 286 AsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnAsnSerLysTrpLysThr 305
 Db 243 AACCTTTATGTTAAGAGTTTGTGATGAACCTCAAAAACAATAATTCCTAAGTGGAGAGCC 302
 QY 306 TyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAsp 325
 Db 303 TATAAGGAATGTTGAATAATGAAGAAAGGTGTTTCAGGGTAACCTTAACCTTCGGGAC 362
 QY 326 ProValGlnAsnAsnPheIleProPheIleValAlaArgTyrValArgValProGln 345
 Db 363 CCAGTGCAGAAACAATTTTCATCCCTCCATCGTGGCCAGATATGCGGGTGTGCCCCAG 422
 QY 346 ThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGlnGly 365
 Db 423 ACATGGCACCAGAGATAGCCTTAGAGGTGGAGCTCATTTGGTTCACAGATTACACAAAGT 482
 QY 366 AsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLysGlu 385

DB:	4	Gaps:	1
US-10-813-588-2 (1-487) x AK016485 (1-1924)			
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QY	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	322	ACAGTCCCAAGGGAGAGACTTATCTGAGGTGGGAGATTGGAACATTGAGTCCCAAG	381
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DB	382	ACCTGCGCTTCTGACTATCTCTCTTCAGCAGTGCACAGCATCATGATGCTCCATATTGT	441
QY	61	GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
DB	442	GGGAGTTGGGCTGTTCCTCCAAAGAACTCCGGCTGAACCTCAACGGAAGTGACTGCTCTTC	501
QY	81	SerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	502	AAGAGTGGATCTACATTTCTTGGCGGGGCTTTCTGCTGACCTACGCCAGCAGTGACCAT	561
QY	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
DB	562	CCGATTTTAATAACCTGTTTGGACGAGGAGCCCATTTATTTCCGAGGAAAAATACAGCAA	621
QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
DB	622	TTCTGCCAGCTGGCTGTAGAGACATGACGAGAGATATTTCTGGGAATACAAAGATGGT	681
QY	141	TyrArgAspThrSerLeuLeuCysLysAlaIleHisAlaGlyIleIleAlaAspGlu	160
DB	682	TACAGATACCTCTTTATTTGTGCAAGTGCATCCACGAGGATCATCACAGATGAA	741
QY	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
DB	742	CTAGGTGCCACATCACTGCTTTTCAGACGAAAGGATAGTCACTATGAGGACTCCTG	801
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	802	GCCAAATGCGTGTCTCCCGCATGGTCTTTGTGCGAAAGCATTTCTTTT	855
QY	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	855	-----	855
QY	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
DB	855	-----	855
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu	260
DB	855	-----	855
QY	261	TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer	280
DB	855	-----	855
QY	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn	300
DB	855	-----	855
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
DB	855	-----	855
QY	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340
DB	855	-----	855
QY	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys	360


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QY 281 ThrGlnSerAsnPheAsnPhetYrVallySerPheValMetAsnPhelYsAsnAsn 300
Db 667 ----- 667
QY 301 SerLysTrpLysThrTyrLysGlylleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 667 ----- 667
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
Db 667 ----- 667
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 667 ----- 667
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 667 ----- 667
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 668 -----ACACCCCA 676
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
Db 677 GGAATGAATATTACAACTGTGGGATTCATCAGTGATCTTCATCGCCCTCTCTGACT 736
QY 421 GlyMetGlyIlePheAlaIlePheArgLysLysLysLysLysGlySerProTyrGlySer 440
Db 737 GGAATGGGGATCTTTGCAATCTGTAGAAAGAGGAAAAAGAAAGAAATCCATATGTGTCA 796
QY 441 AlaGluAlaGlnLysThrAspCysTTPlysGlnIleLysTyrProPheAlaArgHisGln 460
Db 797 GCTGAGCTCAGAAACAGGCTGTGGAGAGAGATTAATATATCCCTTTCCAGGCAATCAG 856
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 857 TCGACGGAATTTACCATCAGCTATGACATGAAAGAGATGACACAAAGTTGGATCTC 916
QY 481 IleThrSerAspMetAla 486
Db 917 ATCACTAGTAGATGGCA 934
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RESULT 7
CN404610 652 bp mRNA linear EST 16-MAY-2004
LOCUS 1700532579818 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN404610
ACCESSION CN404610.1 GI:47392155
VERSION EST.
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 652)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,X., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 652 Std Error: 0.00.
Location/Qualifiers
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FEATURES

RESULT 8
DN134443
LOCUS

DEFINITION 999656 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION DN134443
VERSION DN134443.1 GI:59828760

source

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1. .652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="Oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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ORIGIN

```
Alignment Scores:
Pred. No.: 3 85e-115 Length: 652
Score: 1154.00 Matches: 217
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.13% Indels: 0
DB: 7 Gaps: 0
US-10-813-588-2 (1-487) x CN404610 (1-652)
QY 120 LysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAsp 139
Db 1 AAATTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGAATATGGTAGAT 60
QY 140 GlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAsp 159
Db 61 GGATATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCGAGGAATAATTGCTGAT 120
QY 160 GluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIle 179
Db 121 GAACTAGGTGGCCACATCAGTGTGTTTTCAGCCCAAGGGATCAGTCGATATGAGGGATT 180
QY 180 LeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThr 199
Db 181 CTGGCCAAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACC 240
QY 200 SerAsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 219
Db 241 TCCAAATGGTTGCAGCAGATCTCTTGAGTTTGAACCTGACGGGCAATTCAGAGCTCTTCC 300
QY 220 SerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArg 239
Db 301 TCATGGCAGTCCGTCATGAGAGTGGAGACCAGTTCACTGGTCTCTCTGCCCACGCCGA 360
QY 240 LeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArg 259
Db 361 CTTCAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACAACCAACCAACCA 420
QY 260 GluTrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrGly 279
Db 421 GAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAATAACAGGAATTAGGACCAACAGGA 480
QY 280 SerThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPhelYsAsnAsn 299
Db 481 TCTACACAGTCGAACTTCACTTTTATGTTAAGATTTTGTGATGATCAATTCAAAACAAT 540
QY 300 AsnSerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGly 319
Db 541 AATTCTAGTGAAGACCTATTAAGGAATTTGGAATAATGAAGAAAGGTGTTTCAGGT 600
QY 320 AsnSerAsnPheArgAspProValGlnAsnAsnPheIleProProIleVal 336
Db 601 AACTTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCCATCGTG 651
```


Email: genome-resseqc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers
 1..956
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strains="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4631413K11"
 /sex="mixed"
 /tissue_type="skin"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 0 day neonate
 skin"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 100.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATTCGAGTTAATTAATTCCTCCCCCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda FLC I"

ORIGIN

Alignment Scores:

Pred. No.:	1.15e-86	Length:	956
Score:	896.00	Matches:	202
Percent Similarity:	47.95%	Conservative:	32
Best Local Similarity:	41.39%	Mismatches:	52
Query Match:	35.04%	Indels:	203
DB:	5	Gaps:	2

US-10-813-588-2 (1-487) x BY713935 (1-956)

Qy 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
 Db 69 ATGACATCTAAGATTATCCAGGGGACTTACCCCAATTACACTGTGTGTGAAGATCATC 128

Qy	21	ThrValProLysGlyLysArgLeuLeuArgLeuGlyAspLeuAspIleGluSerGln	40
Db	129	ACAGTCCCAAGGGGAAGAGACTTATCTGAGTTGGGAGATTGAACATTAGTCAAG	188
Qy	41	ThrCysAlaSerAspTyrIleLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys	60
Db	189	ACCTCGGCTTCTGACTATCTCTCTTCAGCAGTGCAACAGATCAGTATGGTCCATATTGT	248
Qy	61	GlySerMetThrValProLysGluLeuLeuAsnThrSerGluValThrValArgPhe	80
Db	249	GGGAGTTGGCTGTTCCCAAGAACTCCGGCTGAACTCAACGGAAGTACTGTCTCTTC	308
Qy	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
Db	309	AAGAGTGGATCTCACAATTTCTGCCCGGGCTTCTGCTGACCTACGCCAGCAGTGACCAT	368
Qy	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
Db	369	CCAGATTTTAAATACCTGTTTGGACGAGGAGCCCATTTATTCGAGGAAAAATACAGCAAA	428
Qy	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerClyAsnMetValAspGly	140
Db	429	TTCTCCCGCAGCTGGCTGTAGACATAGCAGAGATATTTCTGGGAATACAAAAGATGTT	488
Qy	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu	160
Db	489	TACAGAGATACCTCTTTATTGTGCAAGCTGCATCCACGCGGATCATCACAGATGAA	548
Qy	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
Db	549	CTAGGTGGCCACATCAACTTGCTTCAGACAAAGGATAAGTCACTATAGAGGACTCCTG	608
Qy	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
Db	609	CTCAATGGCGTCTCTCCGCGCATGCTTTCTTGTGCGAGAGCGATTTCTTTT	662
Qy	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
Db	662	-----	662
Qy	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
Db	662	-----	662
Qy	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu	260
Db	662	-----	662
Qy	261	TrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGlySer	280
Db	662	-----	662
Qy	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn	300
Db	662	-----	662
Qy	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
Db	662	-----	662
Qy	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340
Db	662	-----	662
Qy	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys	360
Db	662	-----	662
Qy	361	GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal	380
Db	662	-----	662
Qy	381	SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr	400


```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 770)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDA375 row: a column: 16
High quality sequence stop: 607.
Location/Qualifiers
1. 770
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30342255"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:"
FEATURES
source

```

all-XhoI; Site 2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 8,76e-82 Length: 770
Score: 850.00 Matches: 166
Percent Similarity: 98.22% Conservatve: 0
Best Local Similarity: 98.22% Mismatches: 1
Query Match: 33.24% Indels: 2
DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x CB988462 (1-770)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 268 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACACTCTTTGGGAAGACAAAT 327
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 328 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCGAG 387
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 388 ACCTGTGCTTCTGACTATCTCTCTCCACAGCTCTTCAGATCAATATGTCATCTACTGT 447
QY 61 GlySerMetThrValProLysGluLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 448 GGAAGTATGACTGTTCCCAAGAACTCTCTTGACACAGTGAAGTAACCGTCGCTTT 507
QY 81 GluSerGlySerHisLeuSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 508 GAGAGTGGATCCACATCTTCTGGCCGGGTTTCTTGCTGACCTATGCGAGCAGCCAT 567
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 568 CCAGATTATACATGTTTGGAAAGCTAGCTAGCCATATTATTGAAGACAGAAATACGCAA 627
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspG1 140
DB 628 TTCTGCCAGCTGGTTGATAGAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGG 687
QY 140 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleAlaAspG 160
DB 688 ATATAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAAGGAATAATTGCTGATG 747
QY 160 IuLeuGlyGlyGlnIleSerVal 167
DB 748 AACTAGTGGCCAGATCATTTGTG 770

RESULT 13

DR845229 864 bp mRNA linear EST 29-JUL-2005
LOCUS JGI_CABE10279.fwd NIH_XGC_tropOval Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7828804 5', mRNA sequence.

ACCESSION DR845229.1 GI:71501083
VERSION
KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM

Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE

1 (bases 1 to 864)
Richardson, P., Lucas, S., Rokhsar, D., Dettter, J. C., Ng, D. C.,
Brockstein, P. and Lindquist, E. A.

TITILE

DOE Joint Genome Institute Xenopus tropicalis EST project

JOURNAL
COMMENT

Unpublished (2004)
Other ESTs: JGI_CABE10279.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 236 5600
Fax: 925 236 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNLN:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CABE 0105 row: n column: 2
High quality sequence stop: 766.

FEATURES
source

1..864
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"
/clone="IMAGE:7828804"
/sex="Female"
/tissue_type="Ovary"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
/clone_lib="NIH_XGC_tropOval"
/note="Vector: pCSI07; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from 5 ug of poly A+ RNA by oligo-dT
priming
(5'-ACTAGTGGCGCGCTAGCTCGAGTTTCTTTTCTTTTCTTTT-3') and
Stratascript reverse transcriptase. After ligation of
EcoRI adapters (5'-AATTCGACGAG-3') followed by kinasing
adapters and by XhoI digestion, the cDNA was size selected
by chromatography on Sepharose CL-2B columns and fractions
containing cDNAs larger than 1000 bp were ligated into
EcoRI/XhoI-digested pCSI07. Reference for library
construction: Current Genomics 4, 635-644. Library
constructed by Michelle Jabb and Bruce Blumberg (Dept of
Developmental and Cell Biology, University of California,
Irvine)."

ORIGIN

Alignment Scores:
Pred. No.: 2.01e-78 Length: 864
Score: 820.00 Matches: 163
Percent Similarity: 75.00% Conservatve: 38
Best Local Similarity: 60.82% Mismatches: 57
Query Match: 32.07% Indels: 10
DB: 6 Gaps: 6

US-10-813-588-2 (1-487) x DR845229 (1-864)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 74 CTAACTCTAAGAAATATCCCTGGACATACCCCTAACCAACACTTTGTAAATAACTCTC 133
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 134 AAAGTACAAACTGGCAAAAGCCTCTATATTATGCTGGCAGATGTAGACATAGAAATCTCGG 193
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyPro 58
DB 194 GATTGTGAATCGGCATATCTTGAAAGAACTCTTAAGGAACTTCATCTGAGGAGATGCTAGC 253
QY 59 TyrCysGlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 77
DB 254 TACTGTGGAGATCAGAAACTATATACCAAGAAATGCTCTTGAATACCAATGAAGCCACC 313

QY 78 ValArgpHeGluSerGlySerHisIleSerGlyValArgGlyPheLeuLeuThrTyrAlaSer 97
 :::
 Db 314 ATCCACTTTGAGAGTGAATTCATGCTGCTGAGCGTGATTTTGTCTTAACGACGACG 373
 QY 98 SerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIleThrGlu 117
 Db 374 AGTGATCATCCAGATCTGATAACATCGCTGGCAAGATCTTAATCATTTATAAGACATAGAA 433
 QY 118 TyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAenMet 137
 Db 434 TACAGCAGATTTCTGTCACGCTGTTCCAAAGATGTAGCTGGGATATCTCAGAGATGTG 493
 QY 138 ValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIle 157
 Db 494 GTGGAAGGATACAGATACCTCTGCTTTCGAAAGCTGGCATTCATCTGGAGTATT 553
 QY 158 AlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGlu 177
 Db 554 GCAGATGAATCTGGGGGACAGATTCAGGTGAACACGACCAAAAGGTATCAGCCGATACAGA 613
 QY 178 GlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeu 197
 Db 614 GGCCTTCTGGCAACGCGCATCTGTCCAAAGATGGGTCTCTTCAGACCATCGGGTGTG 673
 QY 198 PheThrSerAsnGlyCysSerArgSerLeuSer-----PheGluProAspGlyGlnIle 215
 Db 674 TTTAGAGGCTCTGACGCTGAGCTATCTTGACGCTGGGGTTCGAAAGAT---AAGTTT 730
 QY 216 ArgAlaSerSerSerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerPro 235
 Db 731 TCAGGCACCTCTCTTATCACTGGAACAGCTGAAACAGGGGAGATTAAAGTCTTGGTGCCT 790
 QY 236 GlyGlnAlaArgLeuGlnGlyProSerTrpAlaSerGlyAspSerSerAenAen 255
 Db 791 GAAAGAGCACAGCTTAAACACAGAGCATTTCTCGGGCTTCTGATCACCAGTCCAGT--- 847
 QY 256 HisLysProArgGluTrpLeuGlu 263
 Db 848 -----CGGGATGTTAGAA 862

RESULT 14
 CN440576
 LOCUS
 DEFINITION BE04022B1F09 BE04 Normalized and Subtracted bovine embryonic and extraembryonic tissue Bos taurus CDNA clone BE04022B1F09 5', mRNA sequence.
 ACCESSION CN440576.1 GI:46419840
 VERSION
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE
 AUTHORS Lewin,H.A., Renard,J.P., Yang,X.J., Hernandez,A., Degrelle,S., Hue,I., Tian,X.C., Liu,L. and Everts,R.E.
 TITLE Bovine embryonic ESTs
 JOURNAL Unpublished (2004)
 COMMENT Department of Animal Sciences
 University of Illinois at Urbana-Champaign
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 Email: h-lewin@uiuc.edu
 Funding for embryonic EST sequencing was provided by USDA ARS
 Contract No. 58-1275-2-020 to H. A. Lewin. Base Calling/Quality
 Scores: PHRED from Washington University Genome Center. Vector
 Trimming: Cross_match from Washington University Genome Center
 PHRAP suite. Sequences submitted are vector free and at least 200

' bp in length with average PHRED score > 20.
 PCR PRIMERS
 FORWARD: CCAGTCACGACCTGTAAACGAC (M13 NIA-F)
 BACKWARD: GTGTGGATTTGTGCGGATACAA (M13 NIA-R)
 Insert length: 830 Std Error: 0.00
 Plate: BE04022B1 row: F column: 09
 Seq primer: TAATGACACTCATATAGG (T7 PROMOTER)
 High quality sequence stop: 830.

FEATURES

source
 1..830
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BE04022B1F09"
 /tissue_type="embryo (day 36 and day 64) and extra-embryonic tissue (day 14 to 25) Normalized and twice substracted library"
 /lab_host="DH10B"
 /clone_lib="BE04 Normalized and Subtracted bovine embryonic and extraembryonic tissue"
 /note="Vector: pGEMZf1(+); Site 1: EcoRI; Site 2: NotI; The cDNA library was constructed, normalized and substracted by Dr. A. Hernandez, W.M. Keck Center, University of Illinois Urbana-Champaign and S. Degrelle, BDR, Institut National de la Recherche Agronomique, France, as described in Bonaldo, M.P., Lennon, G. and Soares, M.B. (1996) Genome Research 6(9): 791-806. This clone is from library BE04, a normalized library of embryonic tissues substracted with 7800 known placental EST sequences and 5000 clones from the BE03 library. The double stranded cDNA was size selected (more than 450 bp), adaptored with EcoRI adaptors at both ends and then digested with NotI. The cDNA was then directionally cloned into EcoRI-NotI digested pGEM11zf(+) phagemid vector. Insert size was between 450-2200 bp. Sequencing was done from the 5' end of the clone. Tagged oligo-dT was used to identify the source of the ESTs where possible. (A18)TGGGT = extraembryonic tissue; (A18)TCGGT = 36-day old fetus; (A18)TCGGA = 64-day old fetus (organs); (A18)TCGGA = 64-day old fetus (body)"

ORIGIN

Alignment Scores:
 Pred. No.: 1..75e-76 Length: 830
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 Percent Similarity: 88.44% Conservative: 19
 Best Local Similarity: 78.89% Mismatches: 18
 Query Match: 31.36% Indels: 6
 DB: 7 Gaps: 2

US-10-813-588-2 (1-487) x CN440576 (1-830)

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 Db 1 TTTGTAACTGAACCTCAGAAACAACTCCAAGTGGCAATCTCTATAAGGAATTGTGAAT 60
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 QY 332 IleProIleValAlaArgTyrValArgValValProGlnThrTrpHisGlnArgIle 351
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 QY 352 AlaLeuLysValGluLeuIleGlyCysGlnIle-----ThrGlnGlyAenAen 367
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 QY 368 SerLeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLysGluAenGlu 387
 Db 241 TCACGTGGTGGGACAA--ACAAAGTGTGAATCTGTTGGTTCACGAAAGAGGAATAG 298
 QY 388 ThrIleThrArgProIleProSerGluGluThrSerThrGlyIleAenIleThrThrVal 407

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 17:51:33 ; Search time 726 Seconds

(without alignments)
4470.668 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNYPGTPNHTVCEKTI.....YDNEKEMTQKLDITSDMAG 487

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV-xlp

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2557	100.0	1761	4	AAS00614 Novel hum
3	2557	100.0	1761	11	Adn39765 Cancer/an
4	2557	100.0	1768	4	AAS00613 Novel hum

5	2557	100.0	2010	11	ADN39764	Cancer/an
6	2557	100.0	2010	13	ADR46610	Cancer-as
7	2557	100.0	2010	13	ADR46611	Cancer-as
8	2551	99.8	2145	8	ACD66718	Secreted
9	2551	99.8	2145	12	ADQ10135	Human pol
10	2551	99.8	2888	6	ADT28055	Adi128055 ECMCAD ge
11	2551	99.8	3151	6	ABN86493	Human TAN
12	2551	99.8	3594	4	AAS00660	Human TAN
13	2551	99.8	3594	8	ACD66717	Secreted
14	2551	99.8	3594	12	ADQ10134	Human pol
15	2551	99.8	3676	5	ADL62155	Human ova
16	2512.5	98.3	2547	11	ADN02314	Human CDN
17	2259	88.3	2310	11	ADN39766	Cancer/an
18	2020	79.0	2145	6	ABN86496	Human zcu
19	1322.5	51.7	1265	6	ABN86495	Human CDN
20	1322.5	51.7	1265	6	ABK49565	Human CDN
21	1322.5	51.7	1265	10	ADC29936	Human nov
22	1313.5	51.4	1538	8	ACA10145	Human NOV
23	1313.5	51.4	1538	12	ADO08322	Human NOV
24	1154.5	45.2	2836	6	ABN86494	Mouse zcu
25	1146.5	44.8	1871	3	AAA96736	Polynucle
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29	984	38.5	636	12	ADO08324	Human NOV
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34	860.5	33.7	2280	8	ABX93042	Human LCC
35	860.5	33.7	2328	9	ADA00874	Human ESD
36	860.5	33.7	5657	8	ABX77581	Different
37	860.5	33.7	5657	10	ADJ56259	Human CDN
38	860.5	33.7	6093	10	ADA19345	Human ins
39	860.5	33.7	6595	12	ADQ23685	Human Bof
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45	791.5	31.0	2046	3	AAS251872	Human Fac

ALIGNMENTS

RESULT 1

AAS00615
ID AAS00615 standard; cDNA; 1620 BP.

XX AAS00615;

DT 29-AUG-2001 (first entry)

DE Novel human protein (NHP) DNA sequence #3.

XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1620

FT /*tag= a

FT /product= "Novel human protein #3"

PN WO200129219-A1.

XX 26-APR-2001.

XX 08-OCT-2000; 2000WO-US028798.

XX 19-OCT-1999; 99US-0160285P.

PR 18-FEB-2000; 2000US-0183583P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX WPI; 2001-290917/30.
 DR P-PSDB; AAU00630.
 XX Novel nucleic acid encoding human CUB-domain containing protein, useful
 PT for drug screening, diagnosis and treatment of physiological disorders or
 PT diseases.
 XX Disclosure; Page 28-29; 33pp; English.
 XX The sequence represents a polynucleotide which encodes a novel human
 CC protein (NHP) containing a CUB domain (an extracellular domain). CUB
 CC proteins have been associated with regulating development, modulating
 CC cellular processes and preventing infectious disease. NHP nucleotide
 CC sequences are useful for gene therapy of physiological disorders or
 CC diseases. NHP oligonucleotides are useful as hybridisation probes for
 CC screening libraries and assessing gene patterns. NHP nucleotide sequences
 CC are useful for detecting mutant or inappropriately expressed NHPs (for
 CC example, those proteins associated with obesity, high blood pressure,
 CC connective tissue disorders and infertility) for the diagnosis of a
 CC disease. The polynucleotides may also be used in screening for drugs
 CC effective in the treatment of symptomatic or phenotypic manifestations of
 CC perturbing the normal function of NHP in the body. Nucleotide constructs
 CC encoding NHP products are used to genetically engineer host cells to
 CC express such products in vivo. These host cells allow for the
 CC identification of compounds that bind to NHP receptors or trigger NHP-
 CC mediated pathways
 XX SQ Sequence 1620 BP; 456 A; 353 C; 422 G; 389 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,41e-226 Length: 1620
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-813-588-2 (1-487) x AAS00615 (1-1620)

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 Qy 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
 Db 217 ACAGTACCAAGGGGAAAGACTGATCTCGAGTTGGGAGATTGGGATATCGAATCCAG 276
 Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerSerSerSerSerSerSerSerSer 60
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 Qy 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValAtgPhe 80
 Db 337 GGAAGATGATGCTGTTCCTCAAGAACTCTTGTGTGAACACAAGTGAAGTAAACCGTCCGCTTT 396
 Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuLeuThrTyrAlaSerSerAspHis 100
 Db 397 GAGAGTCGATCCACATTTCTGGCGGGGTTTTTGTGTGACCTATGCGAGCAGCCAT 456
 Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
 Db 457 CCAGATTAAATACATGTTTGGACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAAA 516
 Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 Db 517 TTCTGCCACGCTGTTGTAGAGAGCTAGCAGGAGACATTTCTGGGATATGGTAGATGA 576

Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
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 Qy 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
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 Qy 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
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 Qy 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
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RESULT 4
AAS00613

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ID AC AAS00613;
XX 29-AUG-2001 (first entry)
AC AAS00613;
XX 29-AUG-2001 (first entry)
DE Novel human protein (NHP) DNA sequence #1.
XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ds.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 59..1522
FT /tag= a
FT /product= "Novel human protein #1"
XX WO200129219-A1.
XX 26-APR-2001.
XX 08-OCT-2000; 2000WO-US028798.
XX 19-OCT-1999; 99US-0160285P.
XX 18-FEB-2000; 2000US-0183583P.
XX (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI; 2001-290917/30.
XX P-PSDB; AAU00628.
XX Novel nucleic acid encoding human CUB-domain containing protein, useful
PT for drug screening, diagnosis and treatment of physiological disorders or
PT diseases.
XX Disclosure; Page 30-31; 33pp; English.
XX The sequence represents a polynucleotide which encodes a novel human
CC protein (NHP) containing a CUB domain (an extracellular domain). CUB
CC proteins have been associated with regulating development, modulating
CC cellular processes and preventing infectious disease. NHP nucleotide
CC sequences are useful for gene therapy of physiological disorders or
CC diseases. NHP oligonucleotides are useful as hybridisation probes for
CC screening libraries and assessing gene patterns. NHP nucleotide sequences
CC are useful for detecting mutant or inappropriately expressed NHPs (for
CC example, those proteins associated with obesity, high blood pressure,
CC connective tissue disorders and infertility) for the diagnosis of a
CC disease. The polynucleotides may also be used in screening for drugs
CC effective in the treatment of symptomatic or phenotypic manifestations of
CC perturbing the normal function of NHP in the body. Nucleotide constructs
CC encoding NHP products are used to genetically engineer host cells to
CC express such products in vivo. These host cells allow for the
CC identification of compounds that bind to NHP receptors or trigger NHP-
CC mediated pathways
SQ Sequence 1768 BP; 539 A; 370 C; 421 G; 438 T; 0 U; 0 Other;

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Alignment Scores:

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Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-813-588-2 (1-487) x AAS00613 (1-1768)

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Db 119 ACGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGNATCCAG 178
Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
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Qy 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 239 GGAAGTATGACTTCCCAAGAACTCTTTGTAACACAAAGTGAAGTAAACCGTCCCTTT 298
Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 299 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGACCTATGCGAGCAGCGACCAT 358
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Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 419 TTCTGCCAGCTGCTGTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 478
Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu 160
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Qy 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
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Qy 181 AlaAsnGlyValLeuSerArgAspGlySerIleSerAspLysArgPheLeuPheThrSer 200
Db 599 GCCAATGCTGTTCTTTGAGGGATGGTTTCTGTCAGCAAGCGATTTCTGTTACTCTC 658
Qy 201 AsnGlyCysSerArgSerLeuSerPheLeuProAspGlyGlnIleArgAlaSerSerSer 220
Db 659 AATGGTTGACAGATCTTGTAGTTTGAACCTGACGGCAATCAGAGCTTCTTCTCA 718
Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 719 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACTT 778
Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 779 CAGGACCAAGGCCCATCATGCGCTTCGGCGACAGTAGCAACCAACCAACCGAGAG 838
Qy 261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer 280
Db 839 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATAACAGGATTAGGACCAAGATCT 898
Qy 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 899 ACACAGTCGAACCTTCAACTTTATGTTAAGAGTTTGTGTGAACCTTCAAAAACAATA 958
Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 959 TCTAAGTGGAGACCTATAAGGAATTTGTGAATATGAAGAAAGGTGTTTCAGGGTAAC 1018
Qy 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheValAlaArgTyrVal 340
Db 1019 TCTAACCTTTCGGACCCAGTGCAGAAACAATTTCACTCCCTCCATCGTGGCCAGATATGT 1078
Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1079 CGGGTTGTCCCCAGACATGCGACAGAGTAGCTTGAAGGTGGAGCTCATTTGGTTGC 1138
Qy 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380

Db 1139 CAGATTACACAAGGTAATGATTCAATTGGTGGCGCAAGACAAGTCAAGACCACTGTT 1198
Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1199 TCAACTAAGAAAGAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1258
Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
Db 1259 GGAATAAACATTACAAACGCTGCTATTCCATTGGTGCTCTTTGTTGCTCGTGTGTT 1318
Qy 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
Db 1319 GGAATGGGATCTTTGACGCTTTTGAAGAAGAGAGAGAGAGAGAGAGAGAGATCA 1378
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTrpPheAlaArgHisGln 460
Db 1379 GCGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATAATATCCCTTTCAGACATCAG 1438
Qy 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1439 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1498
Qy 481 IleThrSerAspMetAlaGly 487
Db 1499 ATCACAAGTGATATGCCAGGT 1519
RESULT 5
ADN39764
ID ADN39764 standard; cDNA; 2010 BP.
XX
AC ADN39764;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO: C136.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-039775P.
PR 09-SEP-2002; 2002US-0397845P.
XX
XX (BOSB-) BOS BIOTECHNOLOGY INC.
XX

PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
 XX WPI: 2003-468649/44.
 DR P-PSDB; ADN39981.
 XX
 PT Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 PT a nucleic acid in a biological sample.
 XX
 PT
 XX
 PS Claim 8; SEQ ID NO C136; 1385pp; English.
 XX
 CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a nucleic acid sequence of the invention.
 XX
 SQ Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5, 97e-226 Length: 2010
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0
 US-10-813-588-2 (1-487) x ADN39764 (1-2010)
 QY 1 MetThrSerLysAsnThrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
 DB 282 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAAT 341
 QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
 DB 342 ACAGTACCAAGGGGAAAGAGACTGATCTCAGGTTGGGAGATTTGGATATCGAATCCAG 401
 QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
 DB 402 ACTGTGCTCTGACTATCTCTCTCCACAGCTCTTCAGATCAATATGGTCCACTAGT 461
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
 DB 462 GGAAGTATGACTGTTCCCAAGAACTCTGTTGGAACACAGTGAAGTACCGTCCGCTTT 521
 QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
 DB 522 GAGAGTGGATCCACATTTCTGCGCGGGGTTTTTGTCTGACCTATCGAGCAGCGACCAT 581
 QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
 DB 582 CCAGATTTATATACATGTTTGGAACGAGCTAGCCATATTTTGAAGACAGAAATACAGCAA 641
 QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 DB 642 TTCTGCCAGCTGTTGTAGACGCTAGCAGGAGACATTTCTGGGAAATATGTAGATGGA 701
 QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
 DB 702 TATAGAGATACCTCTTTATTGTGCAAAAGCTGCCATCCATCGAGGAATAATTGCTGATGAA 761

QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 DB 762 CTAGGTGGCCAGATCAGTGTGCTTACGCGAAAGGGATCAGTCGATATGAGGATCTG 821
 QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 DB 822 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTGTACCTCC 881
 QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
 DB 882 AATGGTTGCAGCAGATCCTTGATTTTGAACCTGACGGCAATCATCAGAGCTTCTTCCTCA 941
 QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
 DB 942 TGGCAGTCGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTCGCCCAAGCCGACTT 1001
 QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
 DB 1002 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACAACCAACACCCAGGAG 1061
 QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrGlySer 280
 DB 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAGGACCCACAGGATCT 1121
 QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
 DB 1122 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTCAAAACAATAAT 1181
 QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
 DB 1182 TCTAAGTGAAGACCTATAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1241
 QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
 DB 1242 TCTAACTTTTCGGGACCCAGTCGCAAAACAATTTTCCTCCCATCGTGGCCAGATATGT 1301
 QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
 DB 1302 CGGGTGTCTCCCGACGATGGCCAGAGGATAGCTTGAAGGTGGAGCTCATGTTGCTG 1361
 QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
 DB 1362 CAGATTTACAAAGGTAATGATTTTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCATGTT 1421
 QY 381 SerThrLysGlyGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
 DB 1422 TCAACTTAAGAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1481
 QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
 DB 1482 GGAATAAACATTTACACGGTGGCTATTCATTTGGTGCTCTTGTGTCCTGGTGTGCT 1541
 QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
 DB 1542 GGAATGGGATCTTTGCGAGCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGATGATCA 1601
 QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
 DB 1602 GCAGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTTAAATATATCCCTTTGCGCAGACATCAG 1661
 QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
 DB 1662 TCAGCTGAGTTTACCATTCAGCTATGATATGATGAGAGGAGATGACACAAAGATTGATCTC 1721
 QY 481 IleThrSerAspMetAlaGly 487
 DB 1722 ATCACAAGTGATATGCGAGGT 1742
 RESULT 6
 ID ADN46610
 XX ADN46610 standard; DNA; 2010 BP.

AC ADR46610;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Cancer-associated protein coding sequence, SEQ ID 23.
 XX
 KW Cytostatic; Gene Therapy; cancer; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 126..1745
 FT /tag= a
 FT /product= "Cancer-associated protein, SEQ ID 81"
 FT
 PN WO2004073657-A2.
 XX
 XX 02-SEP-2004.
 XX
 XX 19-FEB-2004; 2004WO-US0005455.
 XX
 XX 19-FEB-2003; 2003US-0448784P.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Aziz N, Gish KC, Wilson KE, Zlotnik A;
 XX
 XX WPI; 2004-652787/63.
 DR P-PSDB; ADR46668.
 XX
 XX
 PT Detecting a pathological cell in a patient for diagnosing or treating
 PT cancer by detecting in a biological sample from the patient genes whose
 PT expression are up-regulated or down-regulated in specific cancers.
 XX
 XX Claim 1; SEQ ID NO 23; 375pp; English.
 PS
 CC The present invention relates to a method for detecting cancer in a
 CC patient. The method comprises detecting in a biological sample from the
 CC patient a nucleotide or protein sequence comprising a sequence that is at
 CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
 CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
 CC cancer for preparing a composition for diagnosing or treating cancer.
 XX
 XX Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 5,97e-226 Length: 2010
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0
 US-10-813-588-2 (1-487) x ADR46610 (1-2010)
 Qy 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThre 20
 Db 282 ATGACATCTAAGAAATTATCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 341
 Qy 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspLeuGln 40
 Db 342 ACAGTACCAAGGGGAAAGAACTGATCTGAGGTTGGGAGATTTCGATATCGAATCCAG 401
 Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
 Db 402 ACCTGTGCTTGTGACTATCTCTCTTCCAGCTCTTCAGATCAATATGTCCTACTGT 461
 Qy 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
 Db 462 GGAAGTATGACTGTTCACAAAGAACTCTTGTGGAACAACAGTGAAGTAACCGTCCGCTTT 521
 Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
 Db

Db 522 GAGAGTGGATCCACATTTCTGCGCGGGGTTTTTGTGCTGACCTATCGAGCAGCGACCAT 581
 Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
 Db 582 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 641
 Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 Db 642 TTCTGCCAGCTGGTTGTAGACAGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 701
 Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
 Db 702 TATAGAGATACCTCTTTATTTGCAAGCTGCCATCCATCGCAGAAATATTTGCTGTATGAA 761
 Qy 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 Db 762 CTAGGTGGCCAGATCAGTGTCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCCTG 821
 Qy 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 Db 822 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTGTTCAGCAAGCGATTTCTGTTCCTCC 881
 Qy 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
 Db 882 AATGTTTCAGCAGATCCTTGATTTTGAACTTCAGCGGCAATATCAGAGCTTCTTCTCA 941
 Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTyrSerProGlyGlnAlaArgLeu 240
 Db 942 TGGCAGTCGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTCGCCAAAGCCGACTT 1001
 Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
 Db 1002 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACACGAGAG 1061
 Qy 261 TrpLeuGluIleAspLeuGlyGluLysLysValThrGlyIleArgThrGlySer 280
 Db 1062 TGCTCGAGATCATTTTGGGGAGAAAAGAAATATACAGGAATTAGGACCACAGGATCT 1121
 Qy 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
 Db 1122 ACACAGTCGAACCTTCACTTTTATGATGAGATTTTGTGATGAATTTCAAAAACAATAA 1181
 Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
 Db 1182 TCTAAGTGGAAAGACCTATAAAGGAATGTGAATTAATGAAGAAAGGTTTTCAGGGTAAC 1241
 Qy 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProIleValAlaArgTyrVal 340
 Db 1242 TCTAATCTTCGGACCCAGTCGAAACAATTTTCATCCCTCCATCGTGGCCAGATATGTG 1301
 Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
 Db 1302 CGGGTTGTCCCCAGACATGGCACAGAGATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1361
 Qy 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
 Db 1362 CAGATTACACAGGTAAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAGACCCAGTGT 1421
 Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
 Db 1422 TCACTTAAGAAAGAGATGAGACATACACAAAGGCCCATCCCTCGGAAGAAACATCCACA 1481
 Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
 Db 1482 GGAATAAACATTACACGGTGGCTATTTCATTTGGTGTCTCTTGTGTCTCTGTTTGTCT 1541
 Qy 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysGlySerProTyrGlySer 440
 Db 1542 GGAATGGGATCTTTTCAGGCTTTTAGAAGAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
 Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
 Db 1602 GCAGAGGCTCAGAAACAGACTGTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1661

QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
 DB 1662 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1721
 QY 481 IleThrSerAspMetAlaGly 487
 DB 1722 ATCACAAGTGATATGCGAGT 1742

RESULT 7

ID ADR46611 standard; DNA; 2010 BP.

XX ADR46611;

XX 18-NOV-2004 (first entry)

XX Cancer-associated protein coding sequence, SEQ ID 24.

DE Cytostatic; Gene Therapy; cancer; human; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 136..1745

FT /tag= a

FT /product= "Cancer-associated protein, SEQ ID 82"

XX WO2004073657-A2.

XX 02-SEP-2004.

XX 19-FEB-2004; 2004WO-US005455.

XX 19-FEB-2003; 2003US-0448784P.

PR (PROT-) PROTEIN DESIGN LABS INC.

PA Aziz N, Gish KC, Wilson KE, Zlotnik A;

XX WPI: 2004-652787/63.

XX P-PSDB; ADR46669.

PT Detecting a pathological cell in a patient for diagnosing or treating
 PT cancer by detecting in a biological sample from the patient genes whose
 PT expression are up-regulated or down-regulated in specific cancers.
 XX Claim 1; SEQ ID NO 24; 375pp; English.

XX The present invention relates to a method for detecting cancer in a
 CC patient. The method comprises detecting in a biological sample from the
 CC patient a nucleotide or protein sequence comprising a sequence that is at
 CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
 CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
 CC cancer for preparing a composition for diagnosing or treating cancer.

XX Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.97e-226 Length: 2010
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-813-588-2 (1-487) x ADR46611 (1-2010)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
 DB 282 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGGCAAGAACAAT 341
 QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40

DB 342 ACAGTACCAAGGGGAAAAAGACTGATTCCTGAGGAGATTGCGATATCGAATCCAG 401
 QY 41 ThrCysAlaSerAspTyrIleuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
 DB 402 ACCTGTGCTTCTGAGCTATCTTCTCTTCCACAGCTCTTCAGATCAATATGGTCCATCTGT 461
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
 DB 462 GGNAGTATGACTGTTCCCAAGAACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 521
 QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuLeuThrTyrAlaSerSerAspHis 100
 DB 522 GAGAGTGGATCCACATTTCTGCGCGGGGTTTTTGTGCTGACCTATCGAGCAGCGACCAT 581
 QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
 DB 582 CCAGATTTAATAACATGTTTGAACGAGCTAGCCATTATTGAAGACAGAAATACAGCAAA 641
 QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 DB 642 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 701
 QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
 DB 702 TATAGAGATACCTCTTATTGTGCAAGCTGCCATCCATGCAGGAATAATTGCTGATGAA 761
 QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 DB 762 CTAGTGGCCAGATCAGTGTGCTTCAAGCAAGGATCAGTCGATATGAAGGATTTCTG 821
 QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 DB 822 GCCAATGGTGTCTTTCGAGGGATGGTTCCTGTCTGACACAGCGATTTCTGTTACTCC 881
 QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
 DB 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGCAAAATCAGAGCTTCTTCTCA 941
 QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
 DB 942 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGCTCTCTCGGCAAGCCCACTT 1001
 QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
 DB 1002 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGACGTAGCAACACCAACCAACAGAG 1061
 QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
 DB 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAGGACCAACAGATCT 1121
 QY 281 ThrGlnSerAsnPheAspPheTyrValLysSerPheValMetAsnPhelyshenAsn 300
 DB 1122 ACACAGTGAACCTTCAACTTTTATGTAAGAGTTTGTGATGAACCTTCAAAACAATAAT 1181
 QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
 DB 1182 TCTAAGTGAAGACCTTAAAGAAATTGTGAATATATGAAGAAAGGTGTTTCAAGGTAC 1241
 QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
 DB 1242 TCTAACTTTCGGGACCCAGTGCACAAATAATTCATCCCTCCCATCGTCCAGATATGTG 1301
 QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
 DB 1302 CGGGTTGTCCTCCACAGATGGCAGAGTAGCCTTGAAGGTGGAGCTCATTTGTTGTC 1361
 QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
 DB 1362 CAGATTACACAGGTAAATGATTCATTTGGTGTGGCGCAGACAAAGTCNAAGCAGCATGT 1421
 QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400

QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTGCTTACGGCAAGGGATCAGTCGATGAGGGATCTG 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 697 GCCAATGGGTGCTTTTCGAGGATGGTTCCTGTGACAGCAAGGATTTCTGTGTAGCTCC 756
QY 201 AsnGlyCySerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 757 AATGGTGTGACAGATCTTTCAGTTTGAACCTGACGGCAATCAGAGCTTCTTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTGGTCAATCAGAGTGGAGACCAAGTTTCACTGTGCTCTTGGCCCAAGCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACACGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB 937 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATAACAGGAATTAGGACCAAGGATCT 996
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 997 ACACAGTCGAACCTTCAACTTTTATGTTTAAAGAGTTTGTGATGAATTTCAAAACATAAT 1056
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGAAGACCTATAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1117 TCTAAGTGGGACCCAGTGCACAAACAATTTCTCCCTCCCAATGTCGCGCATATG 1176
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1177 CGGGTTGTCCTCCCGACATGGCCACGAGGATAGCTTGAAGGTGGAGCTCATTTGTTGC 1236
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTACACAGGTAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCACTGTT 1296
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCAACTAAGAAAGAGATGAGACAATCAAGAGCCCATCCCTCCGGAAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValPheAla 420
DB 1357 GGAATAAACATTACAACGGTGGCTATTCATTGGTGTCTCTTGTCTGCTGGTTGCT 1416
QY 421 GlyMetGlyIlePheAlaPheArgLysLysLysLysGlySerProTyrGlySer 440
DB 1417 GGAATCGGATCTTTTCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1476
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1477 GCAGAGGCTCAGAAACAGACTGTGGAGCAGATTAATATATCTCTTTCGACATCAG 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1537 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGAGATGACACAAAGATTAGATCTC 1596
QY 481 IleThrSerAspMetAla 486
DB 1597 ATCAAGAATGATGGCA 1614

RESULT 9

ADQ10135

ID ADQ10135 standard; cDNA; 2145 BP.

XX

AC ADQ10135;

XX 09-SEP-2004 (first entry)
XX Human polynucleotide #11.
XX Human; gene; ss; cancer; obesity; gastritis; diarrhea; haemorrhoid;
KW asthma; anaemia; graft-versus-host reaction; allergic reaction;
KW cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;
KW osteoarthritis; arteriosclerosis; hypertension; bacterial infection;
KW psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; AIDS; tuberculosis;
KW viral infection; malaria; goiter; infertility; endometriosis;
KW muscular disorder.
XX Homo sapiens.
XX US2004121396-A1.
XX 24-JUN-2004.
XX 19-DEC-2003; 2003US-00741790.
XX 14-JUN-1999; 99US-00333159.
XX 29-JUN-1999; 99US-00342364.
XX 10-SEP-1999; 99US-00393996.
XX 19-OCT-1999; 99US-00420707.
XX 07-JAN-2000; 2000US-00479249.
XX 27-APR-2000; 2000US-00559497.
XX 24-MAY-2000; 2000US-00578063.
XX 16-JUN-2000; 2000US-00596194.
XX 23-JUN-2000; 2000US-00602871.
XX 30-JUN-2000; 2000US-00608452.
XX 12-JAN-2001; 2001US-00759130.
XX (MILL-) MILLENNIUM PHARM INC.
XX Fraser CC, Barnes TM, Sharp JD, KIRST SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADU;
XX WPI; 2004-479675/45.
XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
PT treating cancer, constipation, hemorrhoids, cystic fibrosis,
PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
PT tuberculosis, malaria, goiter, infertility.
XX Claim 2; SEQ ID NO 72; 483pp; English.
XX The invention relates to human polynucleotides and the polypeptides they
CC encode. The invention also relates to a host cell containing a
CC polynucleotide of the invention, an antibody which selectively binds with
CC a polypeptide of the invention, a method of detecting the presence of a
CC polypeptide in a sample, a method of identifying a compound which binds
CC with a polypeptide, and a method of modulating the activity of a
CC polypeptide. The polynucleotides, polypeptides and compositions are
CC useful for diagnosing, preventing and/or treating cancer, obesity,
CC gastritis, diarrhea, haemorrhoids, asthma, anaemia, graft-versus-host
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,
CC infertility, endometriosis, wounds and muscular disorders. This sequence
CC represents a human polynucleotide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX SQ Sequence 2145 BP; 556 A; 561 C; 575 G; 453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,34e-225 Length: 2145
Score: 2551.00 Matches: 486

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.77%	Indels:	0
DB:	12	Gaps:	0

US-10-813-588-2 (1-487) x ADQ10135 (1-2145)			
QY	1	MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGlyLysThrIle	20
DB	157	ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTGGCAAAAGACAAAT	216
QY	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	217	ACAGTACCAGGAGGAGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCG	276
QY	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys	60
DB	277	ACCTGTGCTTCTGACTATCTTCTTCACAGCTCTTCAGATCATATGTCCTCATCTGT	336
QY	61	GlySerMetThrValProLysGlyLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
DB	337	GGAAGTATGACTCTTCCCAAGAACTCTTGTTCACACACAAAGTGAAGTAAACCGTCCGCTT	396
QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	397	GAGAGTGGATCCACACATTTCTGGCGGGGTTTTTGTGACCTATCGAGCAGCGACCAT	456
QY	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
DB	457	CCAGATTAAATACATGTTTGGAAACGAGCTAGGCATTAATTTGAAGACAGATACAGCAA	516
QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
DB	517	TTCTGCCACGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGAAATATGGTAGATGA	576
QY	141	TyrArgAspThrSerLeuLeuLysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu	160
DB	577	TATAGATACCTCTTTATTTGTCNAAGCTGCCATCCATCCAGGAATAATTTGCTGTGAA	636
QY	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
DB	637	CTAGGTGGCAGATCAGTGTGCTTCAGCGCAAGGATCAGTCGATATGAAGGATCTG	696
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	697	GCCAAATGGTGTCTTTTCAGGAGTGGTTCCTGTGCAGCAAGGATTTCTGTATTACCTCC	756
QY	201	AsnGlyCysSerArgSerLeuPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	757	ANTGGTTGCCAGCATCTTGGATTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCA	816
QY	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
DB	817	TGGCAGTCCGTCATAGAGTGGAGACAGTTCACTGGTCTCTCTGCCAAGCCCGACTT	876
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnHisLysProArgGlu	260
DB	877	CAGGACCAAGGCCCATCATGGCTTCGGCGCACAGTAGCAACACCAACCAACACGAGAG	936
QY	261	TrpLeuGluLeuAspLeuGlyGlyLysValLysIleThrGlyIleArgThrThrGlySer	280
DB	937	TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGAAATTAGGACACAGGATCT	996
QY	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnAsn	300
DB	997	ACACAGTCGAACCTCACTTTATTTAGTATGAGTTTGTGATGACTTCAAAACAAATAT	1056
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
DB	1057	TCTAAGTGAAGACCTATAAGGAATTTGTAATTAATGAAGAAAAGGTGTTTCAGGGTAAC	1116
QY	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340

DB	1117	TCTAACTTTCCGGACCCAGTCGAAACAAATTTTCATCTCCCTCCCATCGTGCCAGATATGTG	1176
QY	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuLeuGlyCys	360
DB	1177	CGGGTTGTCCCCAGACATGGCACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC	1236
QY	361	GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal	380
DB	1237	CAGATTACACAAGGTAAATGATTCATTTGGTGGCCGCAAGACAAGTCNAAGCACCAGTGT	1296
QY	381	SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr	400
DB	1297	TCAACTAAGAAAGATGAGACAATCAACAGCCCATCCCTCGGAAGAAACATCCACA	1356
QY	401	GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla	420
DB	1357	GGATAAACAATTCACACGGTGGCTATTCATTTGGTGTCTTGTGTTCTGTTGTTGCT	1416
QY	421	GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLysLys	440
DB	1417	CGAATGGGATCTTTTCAGCCCTTTAGAAAGAAAGAAAGAAAGAAAGAGTCCGTATGATCA	1476
QY	441	AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln	460
DB	1477	GCAGGCTCAGAAACACAGCTGTTGGAAGCAGATTAAATATCCCTTTCCGACATCAG	1536
QY	461	SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu	480
DB	1537	TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC	1596
QY	481	IleThrSerAspMetAla	486
DB	1597	ATCACAAGTGATATGGCA	1614

RESULT	10
AD128055	
ID	AD128055 standard; cDNA; 2888 BP.
XX	
AC	AD128055;
XX	
DT	15-APR-2004 (first entry)
XX	
DE	ECMAD gene clone 184661CB1.
XX	
KW	db; gene; nootropic; antisickling; antianemic; antitumor; anti-HIV;
KW	antiallergic; antianemic; antiasthmatic; immunosuppressive;
KW	antithrombotic; dermatological; nephrotrophic; antigout;
KW	antichryoid; neuroprotective; osteopathic; antipsoriatic; antirheumatic;
KW	antiarthritic; antiulcer; antiinflammatory; ophthalmological;
KW	anticonvulsant; antiparkinsonian; antibacterial; virucide; tranquilizer;
KW	neuroleptic; antidiabetic; cytostatic; hepatotrophic; gene therapy;
KW	human extracellular matrix and cell adhesion molecule; ECMAD; diagnosis;
KW	genetic disorder; adrenoleukodystrophy; Down's syndrome; cystic fibrosis;
KW	Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;
KW	Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;
KW	AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;
KW	atherosclerosis; autoimmune hemolytic anemia; contact dermatitis;
KW	Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;
KW	osteoporosis; psoriasis; rheumatoid arthritis; scleroderma;
KW	systemic lupus erythematosus; ulcerative colitis; uveitis;
KW	neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW	Huntington's disease; Parkinson's disease; multiple sclerosis;
KW	meningitis; periodic paralysis; mental disorder; mood; anxiety;
KW	schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder;
KW	osteoporosis; Paget's disease; osteonecrosis; osteomyelitis;
KW	chondrosarcoma; giant cell tumor; psoriatic arthritis;
KW	infectious arthritis; systemic sclerosis; cell proliferative disorder;
KW	actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer;
KW	adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.
OS	Homo sapiens.
XX	
PN	W0200202634-A2.

QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
 DB 1422 TCAACTAAGAAAGAGATGAGACAATCACAAAGGCCCATCCCTCGGAAGAAACATCCACA 1481
 QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValIleValPheAla 420
 DB 1482 GGAATAAACATTAACAAGGGGTATTTCCATTGGTGCTCTCTGTCTGCTGGGTGCTT 1541
 QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysGlySerProTyrGlySer 440
 DB 1542 GGATGGGGATCTTTGCGAGCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGATCGATGATCA 1601
 QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
 DB 1602 GCAGAGGCTCAGAAACACAGACTGTGGAAGCAGATTAAATATATCCCTTTCGACACATCAG 1661
 QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
 DB 1662 TCAGCTGAGTTTACCATCAGCTATGATATGATGAGAGAGAGATGACACAAAAGTTAGATCTC 1721
 QY 481 IleThrSerAspMetAla 486
 DB 1722 ATCACAAGTGATATGGCA 1739

RESULT 11

ABN86493
 ID ABN86493 standard; cDNA; 3151 BP.

AC ABN86493;

DT 21-OCT-2002 (first entry)

XX Human neurophilin homologue polypeptide, zcub5 encoding cDNA.

XX Neurophilin; zcub5; human; antitumour; antidiabetic; ophthalmological;
 KW antithrombotic; antipsoriatic; antirheumatic; antidiabetic; gene;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW cytosolic; gene therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 76..2223
 FT /*tag= a
 FT /product= "zcub5"

XX WO200253739-A2.

XX 11-JUL-2002.

XX 15-NOV-2001; 2001WO-US045542.

XX 15-NOV-2000; 2000US-0249004P.

XX (ZYMO) ZYMOGENETICS INC.

XX Fox BA, Gao Z, Shoemaker KE;

XX WPI, 2002-590634/63.

XX P-PSDB; ABB81000.

XX Novel isolated neurophilin homolog polypeptide, termed zcub5, useful in
 PT diagnosis or treatment of disorders associated with abnormal cell
 PT proliferation such as cancer and diseases of the nervous system.

XX Example 2; Page 72-77; 101pp; English.

XX The invention relates to an isolated neurophilin homologue polypeptide,
 CC termed zcub5. The polypeptide can be expressed by standard recombinant
 CC methodology. The zcub5 polypeptide and polynucleotide are useful in a
 CC variety of therapeutic, diagnostic and research applications. The
 CC polypeptide is useful for producing antibodies, for imaging tumours or

CC other sites of abnormal cell proliferation, for treating solid tumours,
 CC retinopathies (including diabetic retinopathy and macular degeneration),
 CC atherosclerosis, psoriasis, rheumatoid arthritis and growth factor-
 CC dependent pathologies, to design agonists and antagonists of neurophilin
 CC -semaphorin interactions, for repairing neurological damage due to
 CC stroke, head and spinal injuries, for treating neurodegenerative diseases
 CC such as multiple sclerosis, Alzheimer's disease, and Parkinson's disease,
 CC for mediating development and innervation of stomach tissue, for
 CC identifying, labeling, and isolating selected cell types, as a target for
 CC cell-specific delivery of diagnostic and therapeutic agent, and to
 CC identify inhibitor of zcub5 activity. The zcub5 polypeptide,
 CC polynucleotide and modulators are useful in diagnosis or treatment of
 CC disorders associated with abnormal cell proliferation, including cancer,
 CC impaired or excessive vasculogenesis or angiogenesis and diseases of the
 CC nervous system. The present sequence represents a cDNA encoding the human
 CC zcub5 polypeptide

SQ Sequence 3151 BP; 832 A; 752 C; 824 G; 743 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,02e-225 Length: 3151
 Score: 2551.00 Matches: 486
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.77% Indels: 0
 DB: Gaps: 0

US-10-813-588-2 (1-487) x ABN86493 (1-3151)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
 DB 232 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACATTT 231
 QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
 DB 292 ACAGTACCAAGAGGAAAGAGACTGATTCTGAGTTGGAGATTTGGATATCGAATCCAG 351
 QY 41 ThrCysAlaSerAspTyrIleLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
 DB 352 ACCTGTGCTCTGACTATCTCTCTTCCAGAGCTCTCAGATCAATATGATGTCATACTGT 411
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
 DB 412 GGAAGTATGACTGTTCCCAAGAACTCTTGTGACACAGTGAAGTAACCGTCCGCTTT 471
 QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrLysSerSerAspHis 100
 DB 472 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTGCTGACCTATGCGAGACGACCAT 531
 QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrIleLysThrGluTyrSerLys 120
 DB 532 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 591
 QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 DB 592 TTTCTGCCAGCTGGTTGTAGACAGTACGAGGAGACATTTCTGGGAATATGGTAGATGGA 651
 QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu 160
 DB 652 TATAGAGATACCTCTTTTATTGTCAAAAGCTGCCATCCATGTCAGGAATAATTTGCTGTAA 711
 QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 DB 712 CTAGGTGGCCAGATCATGTGTCTTCAGCGCAAGGATCATGTCGATATGAAGGATTCG 771
 QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 DB 772 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTCAGCAAGCAATTTCTGTTTACCTCC 831
 QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
 DB 832 AATGGTTGCAGACATCTTGTAGTTTTTGAACCTGCGGGCAATTCAGAGCTTCTTCTCTCA 891


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QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 892 TGGCAGTCGGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGGCCCAAGCCGACTT 951
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 952 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACACCAAAACCAGAG 1011
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysLysLysLysLysLysLysLysLys 280
DB 1012 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1071
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1072 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACA 1131
QY 301 SerLysTrpLysTrpLysGlyLysLysLysLysLysLysLysLysLysLysLys 320
DB 1132 TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAA 1191
QY 321 SerAsnPheArgAspProValGlnAsnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1192 TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAA 1251
QY 341 ArgValValProGlnThrTrpHisGlnArgLysLysLysLysLysLysLysLysLys 360
DB 1252 CGGGTTGTCCTCCAGACATGGCACCAGAGAGATAGCCTTGAAGGTGGAGCTCATTTG 1311
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1312 CAGATTACACAAGGTAATGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1371
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1372 TCACTAAGAAAGAGATGAGCAATCAAGAGCCCTCCCTCGGAAGAAATCCACA 1431
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
DB 1432 GGAATAAATACATTACACGGTGGCTATTTCATTGGTGTCTCTGTTGTTGTTGTTGTT 1491
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
DB 1492 GGAATGGGATCTTTGACGCTTTAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTrpPropheAlaArgHisGln 460
DB 1552 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTCCAGACATC 1611
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1612 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGAGATGACACAAAAGTTAGATCT 1671
QY 481 IleThrSerAspMetAla 486
DB 1672 ATCACAAGTGATATGGCA 1689
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RESULT 12

AAS00660
ID AAS00660 standard; cDNA; 3594 BP.

XX AC AAS00660;

XX DT 07-SEP-2001 (first entry)

XX DE Human TANGO 229 cDNA.

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XX Human; TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung;
KW skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
KW bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
KW anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; se;
KW malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
KW attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
KW hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
```

Alignment Scores:

Pred. No.:	4,84e-225	Length:	3594
Score:	2551.00	Matches:	486
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.77%	Indels:	0
DB:	4	Gaps:	0

US-10-813-588-2 (1-487) x AAS00660 (1-3594)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20

DB 228 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTTGCAGAAACAATT 287

QY 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40

DB 288 ACAGTACCAAGGGGAAAGAACTGATTTCTGAGTTGGGAGATTGGATATCGAATCCAG 347

muscular dystrophy; immuno-competence; vertebrate; blood; serum.

Homo sapiens.

Key Location/Qualifiers
CDS 72..2219
/tag= a
/product= "Human TANGO 229"
FT 72..173
/tag= b
FT 174..2216
/tag= c
/product= "Mature human TANGO 229"

WO200129088-A1.

26-APR-2001.

23-JUN-2000; 2000WO-US017386.

19-OCT-1999; 99US-00420707.

(MILL-) MILLENNIUM PHARM INC.

Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby KR;

WPI: 2001-308477/32.

P-PSDB; AAU00670.

New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating cellular processes.

Claim 1; Fig 1; 263pp; English.

The sequence represents a cDNA which encodes human TANGO 229 polypeptide. This protein and similar others exhibit the ability to affect growth, proliferation, survival, differentiation, activity, morphology, or movement/migration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marrow or thymus tissue. They can be used as modulating agents for regulating cellular processes, thus, the proteins and their associated nucleic acids can be used to prognosticate, prevent, diagnose, or treat disorders associated with physiological processes. These disorders include abnormal blood coagulation, asthma, anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohn's disease, gastroenteritis, goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immuno-competent vertebrate and harvesting blood or serum from the vertebrate.

Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

```
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 348 ACCTGTGCTCTGACTATCTCTCTTACCAGCTCTTCAGATCAATATGGTCCATACTGT 407
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 408 GGAAGTATGACTGTTCCCAAGAACTCTTGTGACCAAGTGAAGTAAACCGTCCGCTTT 467
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
Db 468 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTGACCTATCGGAGCAGCGACCAT 527
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 528 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTGGAAGACAGAAATACAGAAA 587
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 588 TTCGCCCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 647
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 648 TATAGAGATACCTCTTTATTGTCAAAAGCTGCCATCCATGCAGCAATATTTGCTGATGA 707
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 708 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCTG 767
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 768 GCCAATGGTGTTCTTTCGAGGGATGGTTCCTGTGCAGACAGGANTTCTGTTCCTCC 827
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
Db 828 AATGGTTGCAGCAGATCCTTGAGTGTGAACTGACGGGCAATACAGAGCTTCTCTCTCA 887
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 888 TGGCAGTTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGCCCAAGCCGACTT 947
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 948 CAGACCAAGGCCATCATCGGCTTCGGGCAAGTACAGTACCAACCAACCAACCAAGAG 1007
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
Db 1008 TGGCTGGAGATCGATTTGGGGAGAGAAAAGAAATAACAGGAATTAGGACCAAGATCT 1067
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 1068 ACACAGTCGAACCTCAACTTTTATGTTAAGAGTGTGATGAACCTTCAAAAAACAATAAT 1127
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
Db 1128 TCTAAGTGGAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1187
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheValAlaArgTyrVal 340
Db 1188 TCTAAGTTCGGGACCCAGTGCAAAACAAATTTTCATCCCTCCATCGTGGCCAGATATGT 1247
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1248 CGGGTTGTCGCCAGACATGCGCACAGAGATAGCTTGAAGGTGGAGCTCATTTGGTTC 1307
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1308 CAGATTACACAGTAATGATTCTTCGTTGGCGCAAGACAGTCAAGACCAAGATGTT 1367
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1368 TCAACTAAGAAAGAAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1427
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValLeuValPheAla 420
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Db 1428 GGAATAAACATTACACGCTGCTATTCCATTGGTGCTCTTGTGTCTGTGTTGCT 1487
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
Db 1488 GGAATGGGGATCTTTTGACGCTTTTAGAAGAAGAAAGAAAGGAGTCCGTATGGATCA 1547
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1548 GCAGAGGCTCAGAAAACAGACTGTTTGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1607
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1608 TCAGCTGAGTTTACCATCAGCTATGATTAATGAAGAGGAGATGACACAAAAGTTAGATCTC 1667
QY 481 IleThrSerAspMetAla 486
Db 1668 ATCACAGTGTATATGGCA 1685

RESULT 13
ACD66717
ID ACD66717 standard; cDNA; 3594 BP.
XX
AC ACD66717;
XX
DT 17-SEP-2003 (first entry)
XX
DE Secreted polypeptide-related cDNA #9.
XX
KW Human; gene; ss; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;
KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW myocardial infarction; congestive heart disease; blood platelet disorder;
KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
XX
OS Homo sapiens.
XX
PN US2003022279-A1.
XX
PD 30-JAN-2003.
XX
PP 12-JAN-2001; 2001US-00759130.
XX
PR 14-JUN-1999; 99US-00333159.
PR 29-JUN-1999; 99US-00342364.
PR 10-SEP-1999; 99US-00393996.
PR 19-OCT-1999; 99US-00420707.
PR 07-JAN-2000; 2000US-00479249.
PR 27-APR-2000; 2000US-00559497.
PR 24-MAY-2000; 2000US-00578063.
PR 16-JUN-2000; 2000US-00596194.
PR 23-JUN-2000; 2000US-00602871.
PR 30-JUN-2000; 2000US-00608452.
XX
PA (FRASER) FRASER C C.
PA (BARN) BARNES T M.
PA (SHAR) SHARP J D.
PA (KIRS) KIRST S J.
PA (MYER) MYERS P S.
PA (LEIB) LEIBY K R.
PA (HOLT) HOLTZMAN D A.
PA (MCCA) MCCARTHY S A.
PA (WRIG) WRIGHTON N.
PA (MACK) MACKAY C R.
PA (GOOD) GOODEARL A D J.
XX
PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KB;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
DR WPI; 2003-456290/43.
DR P-PSDB; ABO32527.
XX
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PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
XX forensic biology.

PS Claim 2; Fig 10A-10P; 482pp; English.

XX The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related cDNA of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,84e-225 Length: 3594
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 8 Gaps: 0

US-10-813-588-2 (1-487) x ACD66717 (1-3594)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 228 ATGACATCTNAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAAAT 287
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 288 ACAGTACCAAGGGGAAAGAGACTGATCTGAGGTGGAGATTGGATATCGAATCCAG 347
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspClnTyrGlyProTyrCys 60
DB 348 ACTGTGCTTCTGACTATCTCTTCCACGAGCTCTTCAGATCAATATGTTCCATCTGT 407
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 408 GGNAGTATGACTGTTCCCAAGACCTCTTGTGACACAGTGAAGTAACCGTCCGCTTT 467
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 468 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTCTGACCTATCCGAGCAGCGACCAT 527
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrIleLysThrGluTyrSerLys 120
DB 528 CCAGATTTTAAATACATGTTTGGAACGAGTAGGCAATTTATTGAAGACAGAAATACAGCAAA 587
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 588 TTCTGCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAAATATGTTAGATGA 647
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu 160
DB 648 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCAGGAATAATTGCTGATGA 707
QY 161 LeuGlyGlyClnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 708 CTAGTGGCCAGATCATGTGCTTTCAGCGCAAGGGGATCAGTCGATATGAAGGGATTCTG 767

QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 768 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTGTCTAGACAGAGGATTTCTGTTTACCTCC 827
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyClnIleArgAlaSerSerSer 220
DB 828 AATGGTTGCAGCAGATCCTTTGAGTTTGAACCTGACGGGCAATATCAGAGCTTCTTCTCTCA 887
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTyrSerProGlyGlnAlaArgLeu 240
DB 888 TGCACGTGGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCAGGCCGACTT 947
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 948 CAGGACCAAGGCCCATCATGGGCTTCGGGGCAGCATGAGCAACCAACCAACCAACGAGAG 1007
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrGlySer 280
DB 1008 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAATAACAGGAATTAGGACCAACAGGATCT 1067
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1068 ACACAGTCAACTTCAACTTTTATGTTAAGAGTTTGTGATGAATTCAAAAACAATAAT 1127
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 1128 TCTAAGTGAAGACCTTAAAGGAATTTGATATATGAGAAAGGTTTTCAGGGTAAAC 1187
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaIleArgTyrVal 340
DB 1188 TCTAATCTTTCGGGACCCAGTCGAAAAACAATTTTCATCCCTCCCATCGTGGCAGATATGTG 1247
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1248 CCGGTTGTCTCCCGACAGCATGGCCAGAGGATAGCCTTGAAGTGGAGCTCATTTGGTTGC 1307
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1308 CAGATTACACAGGTAATGATTCATTTGGTGTGGCGCAGACCAAGTCAGACAGTGT 1367
QY 381 SerThrLysGlyGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1368 TCAACTAAGAAAGAGATGAGACAAATCAACAGGCCCATCCCTCGGAGAAACATCCACA 1427
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValIleValPheAla 420
DB 1428 GGAATAAAACATTACACCGTGGCTATTTCATTTGGTGTCTCTTGTCTGCTGTTGTCT 1487
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLysLys 440
DB 1488 GGAATGGGATCTTTGACGCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1547
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1548 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1607
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1608 TCAGCTGAGTTTACCATCAGCTATGATAATGAAGAGAGATGACACAAAGATTAGATCTC 1667
QY 481 IleThrSerAspMetAla 486
DB 1668 ATCACAAGTGATATGGCA 1685
RESULT 14
ADQ10134
ID ADQ10134 standard; cDNA; 3594 BP.
XX
AC ADQ10134;
XX
DT 09-SEP-2004 (first entry)
XX

DE	Human polynucleotide #10.	DB:	12	Gaps:	0
XX		US-10-813-588-2 (1-487) x ADQ10134 (1-3594)			
KW	Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;	Qy	1	MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle	20
KW	asthma; anaemia; graft-versus-host reaction; allergic reaction;	Db	228	ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACCACCTGTTTGGCAAGACAAAT	287
KW	cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;	Qy	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
KW	osteoarthritis; arteriosclerosis; hypertension; bacterial infection;	Db	288	ACAGTACCAGGCGGAAAGAGCTGATTCGAGTTGGGAGATTTGGATATCGAATCCAG	347
KW	peoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;	Qy	41	ThrCysAlaSerAspTyrIleuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys	60
KW	Huntington's disease; Parkinson's disease; AIDS; tuberculosis;	Db	348	ACCTGTGCTTCTGACTATCTCTCTCACCAGCTCTTCAGATCAATATATGGTCCATCTGT	407
KW	viral infection; malaria; goiter; infertility; endometriosis;	Qy	61	GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	80
XX	muscular disorder.	Db	408	GGAGTATGACTGTTCCCAAGAACTCTTGTGACACAGTGAAGTAACCGTCCGCTTT	467
OS	Homo sapiens.	Qy	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
XX		Db	468	GAGAGTGGATCCACATTTCTGGCGGGGTTTTTCTGCTGACCTATCGAGCAGCAGCAT	527
XX		Qy	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrIleuLysThrGluTyrSerLys	120
XX		Db	528	CCAGATTTAATAACATGTTTGAACGAGCTAGCCATATTTTGAAGACAGAAATACGCAA	587
XX		Qy	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
XX		Db	588	TTCTGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA	647
XX	(MILL-) MILLENNIUM PHARM INC.	Qy	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu	160
XX	Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;	Db	648	TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAGGAATAATTTGCTGATGA	707
XX	Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;	Qy	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
XX	WPI, 2004-479675/45.	Db	708	CTAGGTGGCCAGATCATGTGTCTCAGCCAAAGGATCAGTCGATATGAAGGATCTCG	767
XX	New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and	Qy	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
XX	treating cancer, constipation, hemorrhoids, cystic fibrosis,	Db	768	GCCAAATGGTGTCTTTCGAGGAGTGGTTCCTGTGACAGACGATTTCTGTTCCTCC	827
XX	hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,	Qy	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
XX	tuberculosis, malaria, goiter, infertility.	Db	828	AATGGTTGCAGCAGATCTCTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCTCA	887
PS	Claim 2; SEQ ID NO 71; 483pp; English.	Qy	221	TyrGlnSerValAsnGluSerGlyAspGlnValHisTyrSerProGlyGlnAlaArgLeu	240
XX	The invention relates to human polynucleotides and the polypeptides they	Db	888	TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTTCATCTGCTCTCTGGCCAAAGCCGACTT	947
XX	encode. The invention also relates to a host cell containing a	Qy	241	GlnAspGlnGlyProSerTyrPheSerGlyAspSerSerAsnAsnHisLysProArgGlu	260
CC	polynucleotide of the invention, an antibody which selectively binds with	Db	948	CAGGACCAAGGCCCATCATGGGCTTCGGGCGCAGTAGCAACCAACCAACCAACGAGAG	1007
CC	a polypeptide of the invention, a method of detecting the presence of a	Qy	261	TrpLeuGluIleAspLeuGlyLysLysLysLysLysLysLysLysLysLysLysLysLys	280
CC	polypeptide in a sample, a method of identifying a compound which binds	Db	1008	TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAACAGGATCT	1067
CC	with a polypeptide, and a method of modulating the activity of a	Qy	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnAsn	300
CC	polypeptide. The polynucleotides, polypeptides and compositions are	Db	1068	ACACAGTCGAACCTTCAACTTTTATGTATGAGAGTTTGTGTATGAACTTCAAAAACAATAAT	1127
CC	useful for diagnosing, preventing and/or treating cancer, obesity,	Qy	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
CC	gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host	Db	1128	TCTAAGTGGAGACCTATAAAGGAATTGTGAATAATGAAGAAAAGGTGTTTCAGGGTAAAC	1187
CC	reactions, allergic reactions, cystic fibrosis, hypogonadism,	Qy	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340
CC	cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,	Db	1188	TCTAACTTTTCGGGACCCAGTCGCAAAAACAATTTTCATCTCCCTCCCATCGTGGCCAGATATGT	1247
CC	hypertension, bacterial infections, psoriasis, diabetes mellitus,	Qy	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys	360
CC	hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's				
CC	disease, AIDS, tuberculosis, viral infections, malaria, goiter,				
CC	infertility, endometriosis, wounds and muscular disorders. This sequence				
CC	represents a human polynucleotide of the invention. Note: The sequence				
CC	data for this patent did not form part of the printed specification but				
CC	was obtained in electronic format from USPTO at				
CC	seqdata.uspto.gov/sequence.html.				
XX		SQ	Sequence	3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;	

Alignment Scores:
Pred. No.: 4.84e-225 Length: 3594
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0

Db 1248 CGGGTGTGTCCTCCCGACATGGCCACGAGGATAGCTTGAAGTGCGAGCTCATTTGGTTGC 1307
Qy 361 GlnIleThrGlnGlyAsnSerLeuValTTPArgLysThrSerGlnSerThrSerVal 380
Db 1308 CAGATTACCAAGGTAATGATTCAATGGTGTGGCGCAAGCAAGTCAAGACCAAGTGT 1367
Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1368 TCAACTAAGAAAGAGATGAGACAATCACAGGCCCATCCCTCGGAAGAACATCCACA 1427
Qy 401 GlyIleAsnIleThrThrValIleAlaIleProLeuValLeuValValLeuValPheAla 420
Db 1428 GGAATTAACATTAACAACGGTGGTATTCATTCCTGCTCTCTGCTGCTGCTGCTGCT 1487
Qy 421 GlyMetGlyIlePheAlaIlePheArgLysLysLysLysLysLysLysLysLysLys 440
Db 1488 GGATCGGATCTTTTCAGCCCTTGAAGAAGAAAGAAAGAAAGTCCGTATGATCA 1547
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyxProPheAlaArgHisGln 460
Db 1548 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTCGACACATCAG 1607
Qy 461 SerAlaGluPheThrIleSerTyxAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1608 TCAGCTGAGTTTACCATCAGCTATGATGATGATGATGATGATGATGATGATGATGAT 1667
Qy 481 IleThrSerAspMetAla 486
Db 1668 ATCACAAGTGATATGGCA 1685

RESULT 15

ADL62155

ID ADL62155 standard; DNA; 3676 BP.

XX AC ADL62155;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovarian cancer DNA marker #20367.

XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX OS Homo sapiens.

XX PN WO200170979-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009126.

XX PR 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-0216820P.

XX PR 25-JUL-2000; 2000US-0220661P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lee J, Lillie J;

XX DR WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 20367; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of the
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 3676 BP; 967 A; 841 C; 953 G; 914 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 4.99e-225 Length: 3676
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 5 Gaps: 0

US-10-813-588-2 (1-487) x ADL62155 (1-3676)

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Db 594 CCAGATTTAATAACATGTTTGGACGAGCTAGCCATTATTTGAAGACACAAATACAGCAA 653
Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 654 TTTCTCCCGAGCTGGTGTAGAGACGTAGCAGAGACATTTCTGGGAATATGATGATGA 713
Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleAlaAspGlu 160

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Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
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Qy 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
Db 1074 TGGCTGGAGATCCGATTTGGGGGAGAAAAAGAAATTAACAGGAATTAGGACCACAGGATCT 1133
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Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 1194 TCTAAGTGGAAAGACCTATAAAGGAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAAC 1253
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Db 1494 GGAATAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTCTGGTGGTTTGTCT 1553
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Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1614 GCAGAGGCTCAGAAAAACAGACTGTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1673
Qy 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1674 TCAGTCAGTTTACCATCAGCTATGATATAGAGAAGGAGATGACACAAAAGTTAGATCTC 1733
Qy 481 IleThrSerAspMetAla 486
Db 1734 ATCACAAGTGATATGGCA 1751

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:22:33 ; Search time 6098 Seconds
(without alignments)
4539.646 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557
Sequence: 1 MTSKNYPGTPYHNHVCETI.....YDNEKEMTKLIDITSDMAG 487

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
- Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2557	100.0	1464	6 AR542471	AR542471 Sequence
2	2557	100.0	1464	6 AX118816	AX118816 Sequence
3	2557	100.0	1620	6 AR542473	AR542473 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4	2557	100.0	1620	6	AX118820	Sequence
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6	2557	100.0	1761	6	AX118818	Sequence
7	2557	100.0	1768	6	AR542474	Sequence
8	2557	100.0	1768	6	AX118822	Sequence
9	2557	100.0	2010	6	CQ870614	Sequence
10	2557	100.0	2010	6	CQ870615	Sequence
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12	2551	99.8	2888	6	AX704743	Sequence
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14	2512.5	98.3	2547	6	AX833875	Sequence
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24	892.5	34.9	2846	9	BC026771	Mus muscu
25	874	34.2	489	6	CQ718728	Sequence
26	867.5	33.9	2310	6	AR669813	Sequence
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29	861.5	33.7	4856	9	BC066097	Mus muscu
30	860.5	33.7	2190	6	AX615195	Sequence
31	860.5	33.7	2280	6	AX615194	Sequence
32	860.5	33.7	2328	6	AR669809	Sequence
33	860.5	33.7	2328	6	AR669810	Sequence
34	860.5	33.7	2939	8	AF387547	Homo sapi
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ALIGNMENTS

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LOCUS	AR542471	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
DEFINITION	AR542471	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
ACCESSION	AR542471	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
VERSION	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
KEYWORDS	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
SOURCE	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
ORGANISM	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
REFERENCE	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
AUTHORS	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
TITLE	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
JOURNAL	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
FEATURES	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
source	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
ORIGIN	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
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Score:	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
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Query Match:	100.00%	Indels:	0
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Db	61	ACAGTACCAAGGGGAAAGACTGATCTCAGGTGGGAGATTGGATATCGAATCCAG	120
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Db	121	ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTTTCCAGATCAATATGTCCTACTGT	180
Qy	61	GlySerMetThrValProLysGluLeuLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
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Qy	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu	160
Db	421	TATAGATATACCTTTTATGTGCAAGCTGCCATCCATGACAGAAATATGCTGATGAA	480
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Qy	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
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Qy	261	TrpLeuGluIleAspLeuGlyLysLysLysIleThrGlyIleArgThrThrGlySer	280
Db	781	TGGCTGGAGATCGATTTGGGGGAGAAAGAAATATACAGGAATATGAGCAACAGATCT	840
Qy	281	ThrGlnSerAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn	300
Db	841	ACACAGTCGAATCTCAACTTTTATGTAAAGAGTTTGTGATGAATCTCAAAACCAATAAT	900
Qy	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn	320
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Qy	321	SerAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn	340
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Qy	421	GlyMetGlyIlePheAlaAlaPheArgLysValLysLysLysGlySerProTyrGlySer	440
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Qy	441	AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln	460
Db	1321	GGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTCGACAGATCAG	1380
Qy	461	SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu	480
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ACCESSION	AX118816		
VERSION	AX118816.1	GI:14035774	
KEYWORDS			
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ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and Sands, A.T.		
TITLE	Human cub-domain-containing protein and gene encoding the same		
JOURNAL	Patent: WO 0129219-A 1 26-APR-2001;		
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ORIGIN			
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Score:	2557.00	Matches:	487
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-10-813-588-2 (1-487) x AX118816 (1-1464)			
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Db	1	ATGACATCTAAGAATATATCCCGGACCTACCCCAATCACACTGTTTGCAGAAAGACAAT	60
Qy	21	ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuApilleGluSerGln	40
Db	61	ACAGTACCAAGGGGAAAGACTGATCTCAGGTGGGAGATTGGATATCGAATCCAG	120
Qy	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys	60
Db	121	ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTTTCCAGATCAATATGTCCTACTGT	180
Qy	61	GlySerMetThrValProLysGluLeuLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
Db	181	GGAAAGTATGACTGTTCCTCAAGAACTCTTGTGAACACAAGTGAAGTAACCGTCCGCTTT	240
Qy	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
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Qy	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
Db	361	TTCTGCCCGCTGGTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA	420
Qy	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu	160
Db	421	TATAGATATACCTTTTATGTGCAAGCTGCCATCCATGACAGAAATATGCTGATGAA	480
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Db	481	CTAGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCGT	540
Qy	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
Db	541	GCCAAATGGTGTCTTTCGAGGGATGGTTCCTGTGCAGCAAGCGATTTCTGTTTACCTCC	600
Qy	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
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Qy	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
Db	661	TGGCAGTCGGTCAATGAGGTGGAGACCAAGTTCACCTGCTCTGCGCAAGCCGACTT	720
Qy	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu	260
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QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
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QY 261 TrpLeuGluIleAspLeuGlyLysLysLysIleThrGlyIleArgThrThrGlySer 280
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DEFINITION Sequence 5 from patent US 6743907.
ACCESSION AR542473
VERSION AR542473.1 GI:53934939
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1620)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: US 6743907-A 5 01-JUN-2004;
Lexicon Genetics Incorporated; The Woodlands, TX
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US-10-813-588-2 (1-487) x AR542473 (1-1620)

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LOCUS			
DEFINITION			
Sequence 3 from patent US 6743907.			
1761 bp DNA linear PAT 08-OCT-2004			
Accession AR542472			
Version AR542472.1			
GI:53934938			
Keywords			
Source Unknown.			
Organism Unknown.			
Unclassified.			
REFERENCE			
1 (bases 1 to 1761)			
Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B.			
and Sands, A.T.			
Human proteins and polynucleotides encoding the same			
Patent: US 6743907-A 3 01-JUN-2004;			
Lexicon Genetics Incorporated; The Woodlands, TX			
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Location/Qualifiers			
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QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
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ACCESSION AX118818
VERSION AX118818.1 GI:14035775
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
Human cub-domain-containing protein and gene encoding the same
Patent: WO 0129219-A 3 26-APR-2001;
Lexicon Genetics Incorporated (US)
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US-10-813-588-2 (1-487) x AX118818 (1-1761)
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LOCUS AR542474 1768 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 7 from patent US 6743907.
ACCESSION AR542474
VERSION AR542474.1 GI:53934940
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B.
and Sands, A. T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: US 6743907-A 7 01-JUN-2004;
FEATURES Lexicon Genetics Incorporated; The Woodlands, TX
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Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservatives: 0
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QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 179 ACTGTGCTTCGACTATCTTCTTCAACAGCTCTTCAGATCAATATGGTCCATAGTGT 238
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 239 GGAAGTATGACTGTTCCCAAGAACTCTTTGTTGAACACAAAGTGAAGTAAACCGCTTT 298
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 299 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTCTGCTGACCTATCGGAGCAGCACCAT 358
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QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
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QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
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QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
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Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
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Db 1439 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGAGAGATGACACAAAAGTTAGATCTC 1498
Qy 481 IleThrSerAepMetAlaGly 487
Db 1499 ATCACAAGTGATATGGCAGT 1519

RESULT 8

AX118822
LOCUS AX118822
DEFINITION Sequence 7 from Patent WO0129219.
ACCESSION AX118822
VERSION AX118822.1 GI:14035777

KEYWORDS

Source Homo sapiens (human)

ORGANISM

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE

1 Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
Human cub-domain-containing protein and gene encoding the same
Patent: WO 0129219-A 7 26-APR-2001;
Lexicon Genetics Incorporated (US)

FEATURES

source
1. .1768
Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
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Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x AX118822 (1-1768)

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Db 359 CCAGATTTAATACATGTTTGAACAGAGCTAGCCATTAATTTGAAGACAGAAATACACAAA 418
Qy 121 PheCysProAlaGlyCysArgAepValAlaGlyAepIleSerGlyAsnMetValAepGly 140
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RESULT 9
LOCUS CQ870614 2010 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 23 from Patent WO2004073657.
ACCESSION CQ870614
VERSION CQ870614.1 GI:52000125
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Aziz, N., Gish, K.C., Wilson, K.E. and Zlotnik, A.
TITLE Methods of diagnosis of cancer, composition and methods of
screening for modulators of cancer
JOURNAL Patent: WO 2004073657-A 23 02-SEP-2004;
PROTEIN DESIGN LABS, INC. (US)
FEATURES
source
1..2010
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 5-2e-206 Length: 2010
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x CQ870614 (1-2010)
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Db 282 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTGGCAAGACAATT 341
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Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
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DEFINITION

Homo sapiens discoidin, CUB and LCCL domain containing 1, mRNA
(CDNA clone MGC:46341 IMAGE:5730536), complete cds.

ACCESSION

BC035671 GI:23274238

VERSION

BC035671.1

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

1 (bases 1 to 2010)

AUTHORS

Strausberg,K.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.P., Ziegler,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J., Skalska,U., Smalusz,D.E.,
Mammalian Gene Collection Program Team

CONSRMT

TITLE

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL

PUBMED

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE

12477932

AUTHORS

2 (bases 1 to 2010)

CONSRMT

TITLE

NIH MGC Project
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA

JOURNAL

TITLE

NIH-MGC Project URL: <http://mgi.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov

REMARK

COMMENT

Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 79 Row: i Column: 21

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 27735142.

Location/Qualifiers

1. .2010

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1. .2010

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126. .1745

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ORIGIN

Alignment Scores:

Pred. No.: 5 2e-206 Length: 2010

Score: 2557.00 Matches: 487

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-10-813-588-2 (1-487) x BC035671 (1-2010)

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DB	342	ACAGTACCAAGAGGGAAAGACTGATCTCTGAGGTGGGAGATTGGATATCGAATCCAG	401
QY	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys	60
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QY	61	GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
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QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
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QY	101	ProAspLeuLeuThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
DB	582	CCAGATTATTAACATGTTTGAACAGCTACCTATTTGAAGACAGAAATACACAA	641
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QY	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu	160
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DB	762	CTAGGTGGCCAGATCAGTGTGCTTACGCCAAGGGATCAGTCGATATGAAGGATTCG	821
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Qy 301 SerLysTrpLysThrTyrLysGlyIleValAasnAasnGluLysValPheGlnGlyAasn 320
Db 1182 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAAGAAAGGTGTTTCAGGGTAAC 1241
Qy 321 SerAasnPheArgAspProValGlnAasnAasnPheIleProProIleValAlaArgTyrVal 340
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Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
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Db 1482 GGAATAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTGTTGTCTGGTGTGCT 1541
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LOCUS AX704743 2888 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 47 from Patent WO0202634.
ACCESSION AX704743
VERSION AX704743.1 GI:29561409
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
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REFERENCE
AUTHORS Gururajan, R., Hafalia, A.J., Kallick, D.A., Patterson, C., Azimzai, Y.,
Khan, F.A., Xu, Y., Yao, M.G., Yue, H., Au-Young, J., Batra, S.,
Baughn, M.R., Borowsky, E.A., Lo, T.P., Lu, D.A., Lu, Y., Tang, Y.T.,
Yang, J., Zingler, K.A., Delegeane, A.M., Gietzen, K., Marcus, G.A.,
Nguyen, D.B., Policky, J.D., Ramkumar, J., Thangavelu, K., Walla, N.K.
and Warren, B.A.
TITLE Human extracellular matrix and cell adhesion polypeptides
JOURNAL Patent: WO 020634-A 47 10-JAN-2002;
INCYTE GENOMICS INC. (US)
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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US-10-813-588-2 (1-487) x AX704743 (1-2888)

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Db 522 GAGAGTGGATCCCACTTTCGGCGGGGTTTTTGTGACCTATGCGAGACGAGCAT 581
Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrIleLysThrGluTyrSerLys 120
Db 582 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 641
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QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
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QY 421 GlyMetGlyLysPheAlaLysLysLysLysLysLysLysLysLysLysLysLys 440
Db 1542 GGAATGGGATCTTTCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
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LOCUS CQ413296 3676 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 20367 from Patent WO0170979.
ACCESSION CQ413296
VERSION CQ413296.1 GI:41321077
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 20367 27-SEP-2001;
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source Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Pred. No.: 3,666-205 Length: 3676
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x CQ413296 (1-3676)
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QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
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QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspLysSerGlyAsnMetValAspGly 140
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LOCUS
DEFINITION Sequence 999 from Patent EP1347046.
ACCESSION AX833875
VERSION AX833875.1 GI:39920010
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KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

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REFERENCE

1

Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,

Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,

Tamechika, I., Seki, N., Yoshikawa, I., Otsuka, M., Nagahara, K. and

Masuko, Y.

Full-length cDNA sequences

Patent: EP 1347046-A 999 24-SEP-2003;

Research Association for Biotechnology (JP)

Location/Qualifiers

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source

FEATURES

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Query Match: 98.26% Indels: 2
DB: 6 Gaps: 1
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US-10-813-588-2 (1-487) x AX833875 (1-2547)

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US-10-632-645-14
; Sequence 14, Application US/10632645
; Publication No. US20050276787A1
; GENERAL INFORMATION:
; APPLICANT: Couto, Linda B.
; APPLICANT: Colosi, Peter C.
; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
; FILE REFERENCE: Avigen-04082
; CURRENT APPLICATION NUMBER: US/10/632,645
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/740,211
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/470,618
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/125,974
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/104,994
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 4999
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-632-645-14

Query Match 5.4%; Score 78.4; DB 6; Length 4999;
Best Local Similarity 54.1%; Pred. No. 1.9e-14;
Matches 210; Conservative 0; Mismatches 166; Indels 12; Gaps 2;
QY 696 CTGGTCTCTGGCCAAAGCCGACTTCAGACCAAGCCCATCATGGCTTCGGGCGACAG 755
Db 4396 CTGGTCTCTGCTCAAAAGCTCGACTTCACCTCCAAGG-----GAGGAGTAATGCTGGAG 4449
QY 756 TAGCAACAACCAACCAAGAGTGGCTGGAGATCGATTTGGGGGAGAGAAAGAAAT 815
Db 4450 ACCTCAGGTGAATATCCAAAGAGTGGCTGCAAGTGAGCTTCAGAAACATGAAGT 4509
QY 816 AACAGGAATTAGGACCAAGGACTACACAGTCAAGCTTCAACTTTTATTTAAGAGTTT 875
Db 4510 CACAGGAGTAAGTACTCAGGAGTAAATCTCTGCTTACAGCATGTATGTGAAGGATT 4569
QY 876 TGTGATGAACCTCAAAACATATTTCTAAGTGAAGACCTATAAGGAAATTTGTGAATA 935
Db 4570 CCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGACTCTCTTTT-----TTCAGAAATGG 4623
QY 936 TGAAGAAAAGGTGTTTCAGGGTAACCTAACTTTTCGGGACCCAGTCGACAAACAATTTTCA 995
Db 4624 CAAAGTAAAGGTTTTCAGGGAAATCAAGACTCTTCACACCTGTGGTGAATCTCTCTAGA 4683
QY 996 CCTCCCATCGTGGCCAGATATGTGGGGTTGTCCCCAGACATGGCACCAGAGGATAGC 1055
Db 4684 CCACACCTTACTGACTCGCTACCTTCGAATTCACCCCGAGAGTTGGTGCACCAAGATTGC 4743
QY 1056 CTGAGAGTGGAGCTCATTTGGTTGGCAG 1083
Db 4744 CTTGAGGATGGAGGTTCTGGGCTGGCAG 4771

RESULT 5

US-10-632-645-13
; Sequence 13, Application US/10632645
; Publication No. US20050276787A1
; GENERAL INFORMATION:
; APPLICANT: Couto, Linda B.
; APPLICANT: Colosi, Peter C.
; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
; FILE REFERENCE: Avigen-04082

RESULT 6

US-11-136-527-989/c
; Sequence 989, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 989
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-989
; CURRENT APPLICATION NUMBER: US/10/632,645
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/740,211
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/470,618
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/125,974
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/104,994
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11933
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-632-645-13
Query Match 5.4%; Score 78.4; DB 6; Length 11933;
Best Local Similarity 54.1%; Pred. No. 3.5e-14;
Matches 210; Conservative 0; Mismatches 166; Indels 12; Gaps 2;
QY 696 CTGGTCTCTGGCCAAAGCCGACTTCAGACCAAGCCCATCATGGCTTCGGGCGACAG 755
Db 4371 CTGGTCTCTGCTCAAAAGCTCGACTTCACCTCCAAGG-----GAGGAGTAATGCTGGAG 4424
QY 756 TAGCAACAACCAACCAAGAGTGGCTGGAGATCGATTTGGGGGAGAGAAAGAAAT 815
Db 4425 ACCTCAGGTGAATATCCAAAGAGTGGCTGCAAGTGGACTTCCAGAAACATGAAGT 4484
QY 816 AACAGGAATTAGGACCAAGGACTACACAGTCAAGCTTCAACTTTTATTTAAGAGTTT 875
Db 4485 CACAGGAGTAAGTACTCAGGAGTAAATCTCTGCTTACAGCATGTATGTGAAGGATT 4544
QY 876 TGTGATGAACCTCAAAACATATTTCTAAGTGAAGACCTATAAGGAAATTTGTGAATA 935
Db 4545 CCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGACTCTCTTTT-----TTCAGAAATGG 4598
QY 936 TGAAGAAAAGGTGTTTCAGGGTAACCTTAACCTTCGGGACCCAGTCGACAAACAATTTTCA 995
Db 4599 CAAAGTAAAGGTTTTCAGGGAAATCAAGACTCTTTCACACCTGTGGTGAATCTCTCTAGA 4658
QY 996 CCTCCCATCGTGGCCAGATATGTGGGGTTGTCCCCAGACATGGCACCAGAGGATAGC 1055
Db 4659 CCCACCTTACTGACTCGCTACCTTCGAATTCACCCCGAGAGTTGGTGCACCAAGATTGC 4718
QY 1056 CTTGAGAGTGGAGCTCATTTGGTTGGCAG 1083
Db 4719 CTTGAGGATGGAGGTTCTGGGCTGGCAG 4746

RESULT 6

US-11-136-527-989/c
; Sequence 989, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 989
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-989

APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 8957
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-89

Query Match 4.8%; Score 70.4; DB 6; Length 8957;
Best Local Similarity 49.0%; Pred. No. 1.2e-11;
Matches 190; Conservative 21; Mismatches 165; Indels 12; Gaps 2;
QY 696 CTGGTCTCTGCGCAAGCCGACTTCAGGACCAAGGCCCATCATGCGCTTCGGGGCAGCAG 755
DB 6752 CTRGTCTCTTCAAAAGCTBRACCTTCACTCCCAAGG-----CAGGAGTAATGCTCTGGAG 6805
QY 756 TAGCAACAACCAACCAAGAGAGTGGCTGGAGATCGATTTGGGGAGAGAAAAAAT 815
DB 6806 ACCTYAGRTGAATAATCCAAAAGAGTSKCTGCAAGTGGACTTCCAGAAGACARTGAAAGT 6865
QY 816 AACAGGAATAGGACCAACAGAGTCTACAGAGTGAAGTCACTTCACTTTTATGTTAAGAGTTT 875
DB 6866 CACAGGAGTAATCTCTCRGGGAGTAATAATCTCTGCTTACAGCATGTATGTGAAGAGWK 6925
QY 876 TGTGATGAACCTTCAAAAACAATAATCTTAAGTGGAGACCTATAAAGGAATCTGGAATAA 935
DB 6926 CCTCACTCCAGCAGTCAAGATGCGCATCAGTGGACTCTCTTT-----TTCAAGATGG 6979
QY 936 TGAAGAAAAGTGTTCAGGGTAATCTTAACCTTCGGGACCCAGTGCAGAAAACAATTTCAAT 995
DB 6980 CAAAGTAAAGGTTTTTCAGGGAATCAAGACTCCTTACACACCTGTGTGTAACCTCTCTAGA 7039
QY 996 CCTCCCATCGTGGCCAGATATGCGGGTGTGCCCCAGACATGCGCCAGAGGATAGC 1055
DB 7040 CCAYGTGTACTGACTBRCTASCTTBRAATTCACCCCMGAGTYGGTGCCAGCATTCG 7099
QY 1056 CTTGAAGGTGGAGCTCAATGGTTCAGC 1083
DB 7100 CCTGASGATGGAGGTTCTGCGCTRCGAG 7127

RESULT 10
US-10-995-561-91
; Sequence 91, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 9040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-91

Query Match 4.8%; Score 70.4; DB 6; Length 9040;
Best Local Similarity 49.0%; Pred. No. 1.2e-11;
Matches 190; Conservative 21; Mismatches 165; Indels 12; Gaps 2;
QY 696 CTGGTCTCTGCGCAAGCCGACTTCAGGACCAAGGCCCATCATGCGCTTCGGGGCAGCAG 755

DB 6835 CTRGTCTCTTCAAAAGCTBRACCTTCACTCCCAAGG-----CAGGAGTAATGCTCTGGAG 6888
QY 756 TAGCAACAACCAACCAAGAGTGGCTGGAGATCGATTTGGGGAGAGAAAAAAT 815
DB 6889 ACCTYAGRTGAATAATCCAAAAGAGTSKCTGCAAGTGGACTTCCAGAAGACARTGAAAGT 6948
QY 816 AACAGGAATAGGACCAACAGAGTCTACAGAGTGAAGTCACTTCACTTTTATGTTAAGAGTTT 875
DB 6949 CACAGGAGTAATCTCTCRGGGAGTAATAATCTCTGCTTACAGCATGTATGTGAAGAGWK 7008
QY 876 TGTGATGAACCTTCAAAAACAATAATCTTAAGTGGAGACCTATAAAGGAATTTGTAATAA 935
DB 7009 CCTCACTCCAGCAGTCAAGATGCGCATCAGTGGACTCTCTTT-----TTCAAGATGG 7062
QY 936 TGAAGAAAAGTGTTCAGGGTAATCTTAACCTTCGGGACCCAGTGCAGAAAACAATTTCAAT 995
DB 7063 CAAAGTAAAGGTTTTTCAGGGAATCAAGACTCCTTACACACCTGTGTGTAACCTCTCTAGA 7122
QY 996 CCTCCCATCGTGGCCAGATATGCGGGTGTGCCCCAGACATGCGCCAGAGGATAGC 1055
DB 7123 CCAYGTGTACTGACTBRCTASCTTBRAATTCACCCCMGAGTYGGTGCCAGCATTCG 7182
QY 1056 CTTGAAGGTGGAGCTCAATGGTTCAGC 1083
DB 7183 CCTGASGATGGAGGTTCTGCGCTRCGAG 7210

RESULT 11
US-10-995-561-3575
; Sequence 3575, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3575
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3575

Query Match 3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 926 TTGTGAATATGAAGAAAAGGTTTTCAGGGTAACTTAACTTTCGGGACCCAGTGCAGAA 985
DB 15 TTCAAGATGGCAAGTAAGAGTTTTTCAGGGAATCAAGACTCCTTACACCTGTGGTGA 74
QY 986 ACAATTTCACTCCCTCCCATCGTGGCCAGATATGTCGGGGTCTCCCGGAGATGCGACC 1045
DB 75 ACTCTCTAGACCCACCGTTACTGACTBGTCTACCTCGAATTCACCCCGAGAGTTGGGTGC 134
QY 1046 AGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGCCAG 1083
DB 135 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCAG 172

RESULT 12
US-10-995-561-3786
; Sequence 3786, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

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; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3786
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3786

Query Match      3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy  926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGC AAA 985
Db  10  TTCAAGATGGCAAGTAAAGGTTTTTCAGGGAATCAAGACTCCTTCACACCTGTGTGA 69

Qy  986 ACAATTTTCATCCCTCCCATCGTGCCAGATATGTGCGGTTGTGCCCGACATGGCACC 1045
Db  70  ACTCTCTAGACCCACCGTTACTGACTCGCTTACCTTGAATTCACCCCCAGAGTTGGGTGC 129

Qy  1046 AGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGCCAG 1083
Db  130 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 167

RESULT 13
US-10-995-561-3851
; Sequence 3851, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3851
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3851

Query Match      3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy  926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGC AAA 985
Db  10  TTCAAGATGGCAAGTAAAGGTTTTTCAGGGAATCAAGACTCCTTCACACCTGTGTGA 69

Qy  986 ACAATTTTCATCCCTCCCATCGTGCCAGATATGTGCGGTTGTGCCCGACATGGCACC 1045
Db  70  ACTCTCTAGACCCACCGTTACTGACTCGCTTACCTTGAATTCACCCCCAGAGTTGGGTGC 129

Qy  1046 AGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGCCAG 1083
Db  130 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 167

RESULT 14
US-10-995-561-3853
; Sequence 3853, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3853
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3853

Query Match      3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy  926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGC AAA 985
Db  15  TTCAAGATGGCAAGTAAAGGTTTTTCAGGGAATCAAGACTCCTTCACACCTGTGTGA 74

Qy  986 ACAATTTTCATCCCTCCCATCGTGCCAGATATGTGCGGTTGTGCCCGACATGGCACC 1045
Db  75  ACTCTCTAGACCCACCGTTACTGACTBGCTACCTTGAATTCACCCCCAGAGTTGGGTGC 134

Qy  1046 AGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGCCAG 1083
Db  135 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 172

RESULT 15
US-10-995-561-3984
; Sequence 3984, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3984
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3984

Query Match      3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy  926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGC AAA 985
Db  15  TTCAAGATGGCAAGTAAAGGTTTTTCAGGGAATCAAGACTCCTTCACACCTGTGTGA 74

Qy  986 ACAATTTTCATCCCTCCCATCGTGCCAGATATGTGCGGTTGTGCCCGACATGGCACC 1045
Db  75  ACTCTCTAGACCCACCGTTACTGACTBGCTACCTTGAATTCACCCCCAGAGTTGGGTGC 134

Qy  1046 AGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGCCAG 1083
Db  135 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 172

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:29:37 ; Search time 294 Seconds
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Perfect score: 1464
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 9: /cgn2_6/ptodata/1/ina/backfileseq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1464	100.0	1464	3	US-09-691-344A-1 Sequence 1, Appli
2	1464	100.0	1620	3	US-09-691-344A-5 Sequence 5, Appli
3	1464	100.0	1761	3	US-09-691-344A-3 Sequence 3, Appli
4	1464	100.0	1768	3	US-09-691-344A-7 Sequence 7, Appli
5	449.8	30.7	1871	3	US-09-823-038A-43 Sequence 43, Appli
6	205.8	14.1	2310	3	US-10-191-436A-4 Sequence 4, Appli
7	205.8	14.1	2310	3	US-10-191-436A-6 Sequence 6, Appli
8	204	13.9	2328	3	US-10-191-436A-1 Sequence 1, Appli
9	204	13.9	2328	3	US-10-191-436A-3 Sequence 3, Appli
10	197.8	13.5	2310	3	US-10-191-436A-7 Sequence 7, Appli
11	197.8	13.5	2310	3	US-10-191-436A-9 Sequence 9, Appli
12	94.4	6.4	6893	3	US-09-054-272-37 Sequence 37, Appli
13	94.4	6.4	6914	3	US-09-949-002-6 Sequence 6, Appli
14	94.4	6.4	6987	3	US-09-949-002-231 Sequence 231, App
15	92.8	6.3	6909	2	US-08-804-196-1 Sequence 1, Appli
16	92.8	6.3	6909	2	US-08-858-340-1 Sequence 1, Appli
17	92.8	6.3	6909	3	US-08-746-111-26 Sequence 26, Appli
18	92.8	6.3	6909	3	US-08-454-353A-1 Sequence 1, Appli
19	92.8	6.3	6909	3	US-09-165-019-1 Sequence 1, Appli
20	81.6	5.6	7032	3	US-09-324-867-1 Sequence 1, Appli
21	80.6	5.5	6585	3	US-08-746-111-4 Sequence 4, Appli
22	78.4	5.4	4880	3	US-09-331-793-20 Sequence 20, Appli
23	78.4	5.4	2436	3	US-09-949-016-5790 Sequence 5790, Ap
24	78.4	5.4	4629	2	US-08-484-891-7 Sequence 7, Appli

25	78.4	5.4	4629	3	US-09-150-811-7	GENERAL INFORMA
26	78.4	5.4	4670	3	US-08-717-294-41	Sequence 41, Appl
27	78.4	5.4	4832	3	US-09-001-039B-46	Sequence 46, Appl
28	78.4	5.4	4999	3	US-09-470-618-14	Sequence 14, Appl
29	78.4	5.4	4999	3	US-09-364-862-14	Sequence 14, Appl
30	78.4	5.4	5035	2	US-08-882-083-1	Sequence 1, Appli
31	78.4	5.4	5035	2	US-08-558-107-1	Sequence 1, Appli
32	78.4	5.4	5035	3	US-09-243-539-1	Sequence 1, Appli
33	78.4	5.4	5094	3	US-09-865-022-1	Sequence 1, Appli
34	78.4	5.4	6999	2	US-08-276-594A-1	Sequence 1, Appli
35	78.4	5.4	7056	2	US-08-121-202-1	Sequence 1, Appli
36	78.4	5.4	8241	9	5171844-1	Patent No. 5171844
37	78.4	5.4	8967	2	US-08-366-851A-1	Sequence 1, Appli
38	78.4	5.4	9009	2	US-07-864-004B-3	Sequence 3, Appli
39	78.4	5.4	9009	2	US-08-251-937A-3	Sequence 3, Appli
40	78.4	5.4	9009	2	US-08-212-133A-1	Sequence 1, Appli
41	78.4	5.4	9009	2	US-08-474-503-1	Sequence 1, Appli
42	78.4	5.4	9009	2	US-08-670-707A-1	Sequence 1, Appli
43	78.4	5.4	9009	3	US-09-037-601-1	Sequence 1, Appli
44	78.4	5.4	9009	3	US-09-315-179-1	Sequence 1, Appli
45	78.4	5.4	9009	3	US-09-523-656-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-691-344A-1
; Sequence 1, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/691,344A
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-1

Query Match		100.0%;	Score 1464;	DB 3;	Length 1464;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1464;		Conservative	0;	Mismatches	0; Gaps 0;
QY	1	ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTCGCGAAAGACAATT	60		
DB	1	ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTCGCGAAAGACAATT	60		
QY	61	ACAGTACCAAGGGGAAAGACATGATTCGAGTTCGGAGATTTGGATATCGAATCCCAG	120		
DB	61	ACAGTACCAAGGGGAAAGACATGATTCGAGTTCGGAGATTTGGATATCGAATCCCAG	120		
QY	121	ACCTGTGCTTCGACTATCTTCTTCACAGCTCTTCAGATCAATATGGTCCATATCTGT	180		
DB	121	ACCTGTGCTTCGACTATCTTCTTCACAGCTCTTCAGATCAATATGGTCCATATCTGT	180		
QY	181	GGAAGTATGACTGTTCGCCAAGAACTCTTTGTTGAAACAAAGTGAACACCGTCGCTTT	240		
DB	181	GGAAGTATGACTGTTCGCCAAGAACTCTTTGTTGAAACAAAGTGAACACCGTCGCTTT	240		

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DB 241 GAGAGTGGATCCACAACTTTCTGCGCGGGTTTTTTTGTCTGACCTATGCGAGCAGCGACCAT 300
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QY 361 TTCTGCCACGCTGGTGTAGAGACGTTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
DB 361 TTCTGCCACGCTGGTGTAGAGACGTTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
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DB 421 TATAGAGATACCTCTTTATTTGTGCAAAAGCTGCCATCCATGACAGAAATATTTCTGTGATGAA 480
QY 481 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCGT 540
DB 481 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCGT 540
QY 541 GCCAATGGTGTCTTTTCAGGGATGGTTCCTGTGACAGCAAGGATTTCTGTGTTACCTCC 600
DB 541 GCCAATGGTGTCTTTTCAGGGATGGTTCCTGTGACAGCAAGGATTTCTGTGTTACCTCC 600
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DB 601 AATGGTTGACAGATCCTTTGAGTTTTTGAACCTGACCGGCAAAATCAGAGCTTTCTTCTCA 660
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DB 721 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGAGTAGCAACCAACCAACCAAGAG 780
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DB 781 TGGCTGGAGATCGATTTGGGGAGAAAAGAAATATACAGAAATAGGACCAAGGATCT 840
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DB 841 ACACGTCGAACTTCACTTTTATGTTAAAGTTTGTGATGACTTCAAAACAAATAT 900
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DB 901 TCTAAGTGGAGACCTATAAGGAAATTTGTAATATGAAGAAAGGTGTTTCAGGGTAAC 960
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DB 961 TCTAATCTTTCCGGACCCAGTGCAAAAATAATTCATCCCTCCATCGTGGCCAGATATGTG 1020
QY 1021 CGGGTTGTCCTCCAGACATGGCACCAGAGGATAGCTTTGAAGTGGAGCTCATTTGGTTC 1080
DB 1021 CGGGTTGTCCTCCAGACATGGCACCAGAGGATAGCTTTGAAGTGGAGCTCATTTGGTTC 1080
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DB 1081 CAGATTACAAAGGTATATGATTCAATGGTGTGGCGCAAGCAAGTCAAGGACCAAGTGT 1140
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DB 1141 TCAATTAAGAAAGAGATGAGACAAATCAAGGCCCATTCCTCCGGAAGAAACATCAACA 1200
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DB 1201 GGAATTAACATTACAAAGGTGGCTATTCATTTGGTGTCTCTTGTGTCCTGGTGTGCT 1260
QY 1261 GGAATGGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGGAAAGTCCGTATGGATCA 1320
DB 1261 GGAATGGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGGAAAGTCCGTATGGATCA 1320
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QY 1381 TCAGCTGAGTGTTCACCATCAGCTATGATTAATGAAGAGCAGATGACACAAAAGTTAGATCTC 1440
DB 1381 TCAGCTGAGTGTTCACCATCAGCTATGATTAATGAAGAGCAGATGACACAAAAGTTAGATCTC 1440
QY 1441 ATCACAAGTGATATGCGAGGTTAA 1464
DB 1441 ATCACAAGTGATATGCGAGGTTAA 1464
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RESULT 2

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US-09-691-344A-5
; Sequence 5, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-5
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Query Match 100.0%; Score 1464; DB 3; Length 1620;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 157 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAAAGACAATT 216
QY 61 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCGAG 120
DB 217 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCGAG 276
QY 121 ACCTGTGCTTCTGACTATCTTCTTCCAGAGCTTCCAGATCAATATGTCATCTGT 180
DB 277 ACCTGTGCTTCTGACTATCTTCTTCCAGAGCTTCCAGATCAATATGTCATCTGT 336
QY 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGAAACACAAGTGAAGTAAACCGTCCGCTTT 240
DB 337 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGAAACACAAGTGAAGTAAACCGTCCGCTTT 396
QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTTTGTGACCTATGCGAGCAGGACCAT 300
DB 397 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTTTGTGACCTATGCGAGCAGGACCAT 456
QY 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAAA 360
DB 457 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAAA 516
QY 361 TTCTGCCACGCTGGTGTAGAGACGTTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
DB 517 TTCTGCCACGCTGGTGTAGAGACGTTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 576
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QY 481 CTAGGTGGCCAGATCAGTGTGCTTACGCGAAAGGATCAGTCGATATGAAGGATCTTG 540
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QY 1321 GCGGAGGCTCAGAAAACAGACTGTTTGAAGAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1380
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RESULT 3

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US-09-691-344A-3
; Sequence 3, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-3
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Query Match 100.0%; Score 1464; DB 3; Length 1761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 298 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGCAAGACAAT 357
DB |||||
QY 61 ACAGTACCAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTGGATATCGAATCCCAG 120
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QY 358 ACAGTACCAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTGGATATCGAATCCCAG 417
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QY 121 ACCTGTGCTTGTGATATCTTCTTCCAGCTCTTTCAGATCAATATGGTCCATCTGT 180
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QY 418 ACCTGTGCTTGTGATATCTTCTTCCAGCTCTTTCAGATCAATATGGTCCATCTGT 477
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QY 181 GGAAGTATGATCTTCCCAAGAACTCTTGTGTAACACAGTGAAGTACCGTCCGCTTT 240
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QY 478 GGAAGTATGATCTTCCCAAGAACTCTTGTGTAACACAGTGAAGTACCGTCCGCTTT 537
DB |||||
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QY 538 GAGAGTGGATCCCAATTTCTGCGGGGTTTTTTTGTGCTGACCTATTCGAGCAGCGACCAT 597
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QY 301 CCAGATTTAATAACATGTTTGAACGAGCTAGCCATTTATTTGAAGACAGATAACAGCAA 360
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QY 598 CCAGATTTAATAACATGTTTGAACGAGCTAGCCATTTATTTGAAGACAGATAACAGCAA 657
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RESULT 4

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US-09-691-344A-7
; Sequence 7, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
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; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-691-344A-7

Query Match 100.0%; Score 1464; DB 3; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ACCTGTGCTTTCGACTATCTTCTTCCAGAGCTTTCCAGATCAATATGTCATATCTGT 180
Db 179 ACCTGTGCTTTCGACTATCTTCTTCCAGAGCTTTCCAGATCAATATGTCATATCTGT 238
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACACAAAGTGAAGTAAACCGTCCGCTTT 240
Db 239 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACACAAAGTGAAGTAAACCGTCCGCTTT 298
QY 241 GAGAGTGAATCCACATTTCTGGCCGGGGTTTTTTCGTGACCTATGCGAGCAGACCAT 300
Db 299 GAGAGTGAATCCACATTTCTGGCCGGGGTTTTTTCGTGACCTATGCGAGCAGACCAT 358
QY 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 360
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QY 361 TTTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 420
Db 419 TTTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 478
QY 421 TATAGAGATACCTCTTTATTTGTCAAAGCTGCCATCCATGCAGGAATAATTTGCTGATGAA 480
Db 479 TATAGAGATACCTCTTTATTTGTCAAAGCTGCCATCCATGCAGGAATAATTTGCTGATGAA 538
QY 481 CTAGGTGGCCAGATCAGTGTCTTCAAGCCGCAAGGGATCAGTCGATATGAAGGATCTG 540
Db 539 CTAGGTGGCCAGATCAGTGTCTTCAAGCCGCAAGGGATCAGTCGATATGAAGGATCTG 598
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QY 601 AATGGTTGACAGCAGATCTTGGAGTTTGAACCTTGAACCTTGAACCTTGAACCTTCTCTCA 660
Db 659 AATGGTTGACAGCAGATCTTGGAGTTTGAACCTTGAACCTTGAACCTTCTCTCTCA 718
QY 661 TGGCAGTTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTGCGCCAAAGCCGACTT 720
Db 719 TGGCAGTTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTGCGCCAAAGCCGACTT 778
QY 721 CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGGACCAACCAACCAACCAAGAG 780
Db 779 CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGGACCAACCAACCAACCAAGAG 838
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Db 959 TCTAAGTGAAGACCTTATAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1018
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Db 1259 GGNATTAACATATACACGGTGGCTATTCCATTGGTGCTCTCTGCTGCTGGTGGT 1318
QY 1261 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1319 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1378
QY 1321 GGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCGCAGATCAG 1380
Db 1379 GGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCGCAGATCAG 1438
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1440
Db 1439 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1498
QY 1441 ATCACAAGTGATATGGCAGTTAA 1464
Db 1499 ATCACAAGTGATATGGCAGTTAA 1522

RESULT 5

US-09-823-038A-43
; Sequence 43, Application US/09823038A
; Patent No. 6797271
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compositions Isolated From Stromal Cells
; FILE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1037c3
; CURRENT APPLICATION NUMBER: US/09/823,038A
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Mouse
US-09-823-038A-43

Query Match 30.7%; Score 449.8; DB 3; Length 1871;
Best Local Similarity 84.0%; Pred. No. 1.5e-131;

Matches 508; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTGTTCCGAAAGACAATT 60
Db 193 ATGACATCTAAGAAATTTATCCCGGACCTTACCCCAATTTACACTGTGTTGAAAGATCATC 252
QY 61 ACAGTACCAAAAGGGGAAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 120
Db 253 ACAGTACCAAAAGGGGAAAGAGACTTATTTCTGAGGTTGGGAGATTTTGAACATTTGAGTCCAAG 312
QY 121 ACTGTGCTTCTGACTATCTCTTACCAGCTCTTTCAGATCAATATGGTTCATATCTGT 180
Db 313 ACTGTGCTTCTGACTATCTCTTACCAGCTGCAACAGATCAGTATGGTTCATATCTGT 372
QY 181 GGAAGTATCAGCTGTTCCCAAGAACTCTTTGTTGAAACACAAGTGAAGTAAACCGTCCGCTTT 240
Db 373 GGAAGTATGAGCTGTTCCCAAGAACTCTCGGCTGAACCTCAACGGAAGTGAAGTGTCTCTTC 432
QY 241 GAGAGTGGATCCCAACATTTCTGGCCGGGGTTTTTGTGCTGACCTATTCGAGCAGCAGCCAT 300
Db 433 AAGAGTGGATCTCACATTTCTGGCCGGGGCTTTCTGCTGACCTTACGCCAGCAGTACCAT 492
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGAAA 360
Db 493 CCAGATTTAATAACCTGTTTGGAAACGAGCAGCCATTTATTTCCAGGAAAAATACAGCAA 552
QY 361 TTCTGCCAGCTGTTGTAGAGACGTAGCAGAGACATTTCTGGGAAATATGGTAGATGGA 420
Db 553 TTCTGCCAGCTGTTGTAGAGACGTAGCAGAGATATTTCTGGGAAATACAAAAGATGGT 612
QY 421 TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATTCAGAGAAATAATTTGCTGATGAA 480
Db 613 TACAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCACGAGGATCATCACAGATGAA 672
QY 481 CTAGTGGCCAGATCAGTGTCTTTCAGCCAAAGGGATCAGTCGATATGAAGGGATCTG 540
Db 673 CTAGTGGCCAGATCAACTTGTCTTCAGAGCAAAAGGGATAGTCACTATGAAGGACTCCTG 732
QY 541 GCAATGGTGTCTTTTCAGAGGATGTTCCCTGTGACAGACGATTTCTGTTTACCTCC 600
Db 733 GCAATGGGCTGCTCTCCCGCATGTTCTTTGTGCGAAAGGATTTCTTTTTCACACC 792
QY 601 AATGG 605
Db 793 CCAGG 797

RESULT 6

US-10-191-436A-4
; Sequence 4, Application US/10191436A
; Patent No. 690031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; FILE OF INVENTION: UTILITY OF THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(198)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (199)..(2310)
; FEATURE:

Db 727 GCAGGAGTAGTGTCAAAACACGTTGGGCGGCCAAATCAGTGTGTGTAATAGTAAAGTAT 786
Qy 520 AGTCGATATGAAGGATTCGGCAATGGTGTCTTTTCGAGGAGATGGTTCCCTGTGTCAGAC 579
Db 787 CCTATTATGAAGTCTTTGGCTTAAACAGTCAATCTGTGTGGACACTTATCTACA 846
Qy 580 AAGCGATTTCTGTTTACCTCAATGGTTGCAGAGATCCTTGTAGTTTGTGAACCTGACGG 639
Db 847 AGTCCTTTTACATTTAAGACAAGTGTGTTATGGAACACTGGGGATGGAGTCTGGTGTG 906
Qy 640 -----CAATCAGAGCTTCTTCCTCATGGCAGTCCGTCAATGAGAGTGGAGAC 687
Db 907 ATCCGCGATCCTCAAAATAACAGCATCTCTGTGCTGGAGTGGACTGACCAACAGGGCAA 966
Qy 688 CAAGTTTCACGTGCTCTCTGGCCAAAGCCGACTTTCAGGACCAAGCCCATCATGGGCTTCG 747
Db 967 GAGAACAGTTGGAAACCCAAAGAGCCAGGCTGAAGAACTGACCGCTTGGGCTGCT 1026
Qy 748 GGCAGCAGTAGCAACCAACCAACGAGAGTGGCTGGAGATCGATTTTGGGGGAGAAA 807
Db 1027 TTTGGCCACTGATGAATACC-----AGTGGTTACAAATAGATTTGAATAAGGAA 1074
Qy 808 AAGAAATAACAGGAATTAGGACCAACAGGATCTACACAGTCGAACTTCAACTTTTATGTT 867
Db 1075 AAGAAATAACAGGCATTTAACCACCTGGATCCACCATGGTGGAGCAAAATTAATATGTG 1134
Qy 868 AAGAGTTTGTGTGATGAATTTCAAAAACAATAATCTTAAGTGGAGAGACCTATAAGGAAT 927
Db 1135 TCTGCTACAGATTCCTGTACAGTGATGATGGGAGAAATGGACTGTGTACAGAGCCT 1194
Qy 928 GTGAATAATGAAGAAAGGTGTTTTCAGGGTAACCTTAACTTTCGGGACCCAGTGCAGAAC 987
Db 1195 GGTGTGAGCAAGATAAGATATTTCAAGGAGAAACAAAGATTATCACAGGATGTGCGTAAT 1254
Qy 988 AATTTCATCCCTCCATCGTGGCCAGATATGTGGGGTGTGTCGCCAGACATGGCACCAG 1047
Db 1255 AACTTTTGGCCACCAATTTATGACAGTGTATTTAGAGTGAATCCTACCCAAATGGCAGAG 1314
Qy 1048 AGGATACCTTGAAGGTGGAGCTCATTTGGTTGCCAGATTA 1087
Db 1315 AAAATGCCATGAATGGAGCTCTCGATGTCAAGTTTA 1354

RESULT 10

US-10-191-436A-7

; Sequence 7, Application US/10191436A

; Patent No. 6900031

; GENERAL INFORMATION:

; APPLICANT: Tasuku Honjo

; APPLICANT: Kei Tashiro

; APPLICANT: Kazuhiro Kobuke

; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE

; FILE REFERENCE: Q70993

; CURRENT APPLICATION NUMBER: US/10/191.436A

; CURRENT FILING DATE: 2002-07-10

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 2310

; TYPE: DNA

; ORGANISM: Rattus rattus

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (1)..(198)

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (199)..(2310)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2310)

US-10-191-436A-7

Query Match 13.5%; Score 197.8; DB 3; Length 2310;
Best Local Similarity 53.4%; Pred. No. 1.4e-51;
Matches 477; Conservative 0; Mismatches 392; Indels 24; Gaps 2;

Qy 210 GTTGAACACAGTGAAGTAAACCGTTCGCTTCGAGAGTGGATCCACATTTCTGGCGGG 269
Db 468 GTCCAAAGCAGTGAATCACAGTGTCTGTTCATGAGTGGAAATCATGCTTCTGGTCGAGG 527
Qy 270 TTTTGTCTGACCTATGCGAGCAGCAGCACCATCCAGATTTAAATAACAATGTTTGAACGAGC 329
Db 528 ATTTTGGCTTCTTACTCAGTTATAGATAACAAGATTAAATCATTGTTGGTACTGT 587
Qy 330 TAGCCATATTTGAAGACAGAAATACAGCAAAATCTGCCAGAGCTGGTTGTAGACAGTAGC 389
Db 588 ATCTAATTTTGGAAACCTGAGTTTCAAGTAACTGCCAGCTGGCTGTCTGCTGCTTT 647
Qy 390 AGGAGACATTTCTGGGAATATGCTAGATGATATAGAGATACCTCTTTATTGTGCAAGC 449
Db 648 TGCTGAATATCTGGAAACGATTCCTCATGATATAGAGATTTTCCCGCTGTGTATGGC 707
Qy 450 TGCATCTCCATGCAGGAATAATTTGCTGATGAATAGGTGGCCAGATCAGTGTGCTTCAGCG 509
Db 708 TGGAAATCCATGCAGGAGTAGTGTCAATGTCTGGCTGGCCAAATCAGCGTGTGATTAG 767
Qy 510 CAAAGGAGTCACTGATATGAAGGATTTCTGGCCAAATGTTGTTCTTTCGAGGAGTGGTTC 569
Db 768 CAAAGGCACCCCATATTTACGAAAGTTCTTTTGGCCAAATGTCACTTCCATGGTGGGATA 827
Qy 570 CCTGTCCAGCAAGCGAATTTCTGTTTACCTCCATGTTGCGAGCAGATCCTTTGAGTTTGA 629
Db 828 CTTATCTACAGTCTGTGTTTACATTTAAGACAAGTGTGTTGCTATGGGACTCTAGGATGGA 887
Qy 630 ACCTGACGGG-----CAAAATCAGAGCTTCTTCTCATGGCAGTCCGTCATGA 677
Db 888 GTCAAGTGTGATCGCCGATCCCGAGATAACAGCATCATCTGTGAGTGGACTGACCA 947
Qy 678 GAGTGGAGACCAAGTTTCACTGTCTCTGGCCAAAGCCGAGCTTCAGGACCAAGGCCATC 737
Db 948 CATGGGCGCAGGAGAACAGCTGGAAACCCGAGAGGCGCAGGCTGAGAAAACCGGGGCTCC 1007
Qy 738 ATGGGCTTCGGGCGACAGTAGCAACCAACCAACAGAGAGTGGCTGGAGATCGATTT 797
Db 1008 CTGGGCTGCTTTTGGCCACTGATGAGATC-----AGTGGCTGCAATTTGACCT 1055
Qy 798 GGGGAGAAAGAAATAACAGGAATTAGGACCAAGGATCTACACAGTCCBAATTTCAA 857
Db 1056 TAATAAGGAGAGAGAGATAACAGGCATCGTAAACCACTGGATCTACCTGATAGAGCAAA 1115
Qy 858 CTTTATGTTAAGAGTTTGTGATGAATCTTCAAAAACAATAATTTCTAAGTGGAGACCTA 917
Db 1116 TTACTATGTCTCTGCTTACAGAGTTCGTACAGTACGATGGGCGAGAAATGGACTGTGTA 1175
Qy 918 TAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAACCTTAACCTTTCCGGGACCC 977
Db 1176 CAGAGACCTGTGGCGCTCAGACAGATATTTCAAGGAGAAACAAGATTATCACAAGGA 1235
Qy 978 AGTGCAAAACAATTTTCAATCCCTCCATCGTGGCCAGATATGTGGGGTGTGTCGCCAGAC 1037
Db 1236 TGTTGCTGTAATACTTTTGGCCACCAATTTATGCAAGTTCATTAGAGTGAACCTGTGCA 1295
Qy 1038 ATGGCACCAGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGCCAGATTACAC 1090
Db 1296 GTGGCAACAGAAATTTGCCATGAAGTGGAAATTGCTGGGATGTGAGTTCACTC 1348

RESULT 11

US-10-191-436A-9

; Sequence 9, Application US/10191436A

; Patent No. 6900031

; GENERAL INFORMATION:

; APPLICANT: Tasuku Honjo

; APPLICANT: Kei Tashiro

Db 6386 AATGCCAGGACGCTGTGAATGCTGGCAAGCCAAAGCAAAACAATAAGC-----AG 6439
Qy 781 TGGCTGAGATCGAATTTGGGGGAGAAAAAAGAAATAACAGGAATTAGGACCAACAGGATCT 840
Db 6440 TGGCTAGAAATTCATCTACTCAAGATCAAGAATAACGGCAATTAATACACAGGCTGC 6499
Qy 841 ACACAGTCGAACCTCAACTTTTATGTTAAGATTTTGTGTGATGAACCTTCAAAAACAATAAT 900
Db 6500 AAGTCTCTGCTCTGAAATGTATGTAAGAGCTATACCACTACACTACAGTGAGCAGGGA 6559
Qy 901 TCTAAGTGGAGACCTATAAGGAATTTGTGAATAATGAAGAAAGGTGTTCCAGGCTAAC 960
Db 6560 GTGGAATGGAAACCATACAGGCTGGAATCTCTCAATGTGTGACAGAAATTTTGAAGGAAT 6619
Qy 961 TCTAACTTTCCGGACCCAGTGCACAAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6620 ACTAATACCAAGGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGGTTATC 6679
Qy 1021 CGGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGGTGAGCTCATTTGGTTGC 1080
Db 6680 CGTGTCAATCTTAAACATGGAATCAAAATGTTGCACTTCGCTGGAACTCTTTGGCTGT 6739
Qy 1081 CAGATT 1086
Db 6740 GATATT 6745

RESULT 13
US-09-949-002-6
; Sequence 6, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6914
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-6

Query Match 6.4%; Score 94.4; DB 3; Length 6914;
Best Local Similarity 51.2%; Pred. No. 1.6e-18;
Matches 249; Conservative 0; Mismatches 231; Indels 6; Gaps 1;

Qy 601 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCA 660
Db 6287 AATGGATGTTCCACACCCCTGGGTATGGAATAATGGAAGATAGAAAACAAGCAATCACA 6346
Qy 661 TGGCAGTCGGTCAATGAGTGGAGACCAAGTTCACCTGCTCTGGCCAGCCCGACTT 720
Db 6347 GCTTCTCGTTTAAGAAATCTTGTGGGAGATTAATCTGGGACCTTCCTGCGCCGCTG 6406
Qy 721 CAGGACCAAGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAAGAGAG 780
Db 6407 AATGCCAGGACGCTGTAATGCTGCGCAAGCCAGGCAACCAACAATAAGC-----AG 6460
Qy 781 TGGCTGAGATCGAATTTGGGGGAGAAAAAAGAAATAACAGGAATTAGGACCAAGGATCT 840
Db 6461 TGGCTAGAAATTTGATCTACTCAAGATCAAGAAGATAACGGCAATTAATACACAGGCTGC 6520
Qy 841 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGTGATGAACCTTCAAAAACAATAAT 900
Db 6521 AAGTCTCTGCTCTGGAATGTATGTAAGAGCTATACCACTCACTACAGTGAGCAGGGA 6580

Qy 901 TCTAAGTGGAGACCTATTAAGGAATTTGTAATATGAAGAAAGGTGTTTCAGGCTAAC 960
Db 6581 GTGGAATGGAAACCATACAGGCTGAAATCCTCCATGGTGGCAAGATTTTGAAGGAAT 6640
Qy 961 TCTAAGTTCGGGACCCAGTGCACAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6641 ACTAATACCAAGGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGGTTTATC 6700
Qy 1021 CGGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGGTGAGCTCATTTGGTTGC 1080
Db 6701 CGTGTCAATCTTAAACATGGAATCAAAATGTTGCACTTCGCTGGAACTCTTTGGCTGT 6760
Qy 1081 CAGATT 1086
Db 6761 GATATT 6766

RESULT 14
US-09-949-002-231
; Sequence 231, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 6987
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-231

Query Match 6.4%; Score 94.4; DB 3; Length 6987;
Best Local Similarity 51.2%; Pred. No. 1.6e-18;
Matches 249; Conservative 0; Mismatches 231; Indels 6; Gaps 1;

Qy 601 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCA 660
Db 6135 AATGGATGTTCCACACCCCTGGGTATGGAATAATGGAAGATAGAAAACAAGCAATCACA 6194
Qy 661 TGGCAGTCGGTCAATGAGTGGAGACCAAGTTCACCTGCTCTGGCCAGCCCGACTT 720
Db 6195 GCTTCTCGTTTAAGAAATCTTGTGGGAGATTAATCTGGGACCTTCCTGCGCCGCTG 6254
Qy 721 CAGGACCAAGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAAGAGAG 780
Db 6255 AATGCCAGGACGCTGTAATGCTGCGCAAGCCAGGCAACCAACAATAAGC-----AG 6308
Qy 781 TGGCTGAGATCGAATTTGGGGGAGAAAAAAGAAATAACAGGAATTAGGACCAAGGATCT 840
Db 6309 TGGCTAGAAATTTGATCTACTCAAGATCAAGAAGATAACGGCAATTAATACACAGGCTGC 6368
Qy 841 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGTGATGAACCTTCAAAAACAATAAT 900
Db 6369 AAGTCTCTGCTCTGAAATGTATGTAAGAGCTATACCACTCCATACAGTGAGCAGGGA 6428
Qy 901 TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGCTAAC 960
Db 6429 GTGGAATGGAAACCATACAGGCTGAAATCCTCCATGGTGGCAAGATTTTGAAGGAAT 6488
Qy 961 TCTAAGTTCGGGACCCAGTGCACAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6489 ACTAATACCAAGGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGGTTTATC 6548
Qy 1021 CGGGTTGTCCTCCAGACATCGCACAGAGATAGCTTGAAGGTGAGCTCATTTGGTTGC 1080

Db 6549 CGTGTCTATTCCTAAACATGGAATCAAAAGTATTGCACTTCGCTCGGAACCTTTTGGCTGT 6608
Qy 1081 CAGATT 1086
Db 6609 GATATT 6614

RESULT 15
US-08-804-196-1
; Sequence 1, Application US/08804196
; Patent No. 5874256
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; TITLE OF INVENTION: thrombosis and kit for use with the same.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5874256el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BFO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 948-7400
; TELEFAX: (301) 948-9751
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
US-08-804-196-1

Query Match 6.3%; Score 92.8; DB 2; Length 6909;
Best Local Similarity 51.0%; Pred. No. 5.3e-18;
Matches 248; Conservative 0; Mismatches 232; Indels 6; Gaps 1;
Qy 601 AATGGTTGACAGATCCTTTGAGTTTGAACCTTGACGGGCAATCAGAGCTTCTTCCTCA 660
Db 6280 AATGGATGTTCCACACCCCTGGGTATGGAATAATGGAAGATAGAAACAGCAATCACA 6339
Qy 661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTGTGGCCAAAGCCGACTT 720
Db 6340 GCTTCTTCTGTTAAGAAATCTTGTGGGAGATTACTTGGGAACCTTCGTCGCCGCTG 6399
Qy 721 CAGGACCAAGCCCATCATCGGCTTCGGGGCAGTAGCAACCAACCAACCAACAGAG 780
Db 6400 AATGCCCCAGGAGCGTGTGAATGCTTGGCAAGCCCAAGCAACCAATAGC-----AG 6453
Qy 781 TGGCTGGAGATCGATTGGGGGAGAAAAAGAAATAACAGAAATTAGGACCAAGGATCT 840
Db 6454 TGGCTAGAATTTGATCTACTCAAGATCAAGAGATACGGCAATTATACAGGGCTGC 6513
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAACAATAAT 900

Db 6514 AAGTCTCTGTCCTCTGAAATGTATGTAAAGAGCTATACCATCCACTACAGTGACGAGGA 6573
Qy 901 TCTAAGTGGAGACCTATATAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db 6574 GTGGAATGGAAACCATACACAGGCTGAAATCCTCCATGGTGGACAAGATTTTGAAGGAAAT 6633
Qy 961 TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6634 ACTAATACCAAGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGGTTTATC 6693
Qy 1021 CGGGTTGTCCCCCAGACATGGCACCCAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 6694 CGTGTCAATTCCTAAACATGGAATCAAAGTATTACACTTCGCCCTGGAACTCTTTGGCTGT 6753
Qy 1081 CAGATT 1086
Db 6754 GATATT 6759

Search completed: January 15, 2006, 19:27:31
Job time : 298 secs

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OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:15:02 ; Search time 5449 Seconds
(without alignments)
12570.433 Million cell updates/sec

Title: US-10-813-588-1
Perfect score: 1464
Sequence: 1 atgacatctaaagaattatcc.....caagtgatggcaggttaa 1464

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	869.2	59.4	1031	3	BM558496
2	741.8	50.7	839	6	CF785931
3	665	45.4	3600	4	CR749448
4	658.6	45.0	961	5	BU177739
5	652	44.5	652	7	CN404610
6	506	34.6	866	8	DN134443
7	489.6	33.4	913	6	CD109068
8	477.4	32.6	770	6	CB988462
9	451.4	30.8	1924	4	AK016485
10	451.4	30.8	2835	4	AK014521
11	445	30.4	956	5	BY713935
12	434.2	29.7	466	1	AW390343
13	427.4	29.2	683	5	EX360287
14	424.2	29.0	686	5	EX345014
15	405.4	27.7	798	6	CB960471
16	403.6	27.6	830	7	CN440576
17	394	26.9	736	8	CX755002
18	381.2	26.0	872	2	BG245910
19	356.8	24.4	404	11	DQ039380
20	355.4	24.3	434	1	AW483656
21	355.4	24.3	883	2	BG975603
22	352	24.0	404	11	DQ039381

23	351	24.0	790	6	CB959630
24	348.6	23.8	1150	3	BM805721
25	348	23.8	348	7	CN404612
26	347	23.7	802	6	CD110061
27	335.4	22.9	406	2	BF740455
28	335.2	22.9	478	10	CG521977
29	320.2	21.9	425	10	CZ293584
30	316.6	21.6	462	10	CL639277
31	312.8	21.4	600	5	BU924048
32	310.2	21.2	417	10	CZ293527
33	308.8	21.1	409	10	CZ293317
34	307	21.0	307	11	DQ046261
35	304.4	20.8	402	10	CZ293313
36	304.4	20.8	426	10	CZ293590
37	302	20.6	864	8	DR845229
38	294.2	20.1	745	5	BU449584
39	292.6	20.0	387	10	CG494608
40	290.2	19.8	509	10	CG636450
41	290.2	19.8	865	8	CX498307
42	289	19.7	456	10	CL302514
43	288	19.7	805	8	CX417452
44	285.2	19.5	388	10	CG662488
45	281.8	19.2	710	7	CN404614

ALIGNMENTS

RESULT 1
BM558496
LOCUS AGENCOURT_6559394 NIH_MGC_88 Homo sapiens cDNA clone linear EST 20-FEB-2002
DEFINITION AGENCOURT_6559394 NIH_MGC_88 Homo sapiens cDNA clone linear EST 20-FEB-2002
5' mRNA sequence.
ACCESSION BM558496
VERSION BM558496.1 GI:18801287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1031)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12757 row: k column: 11
High quality sequence stop: 694.
Location/Qualifiers
1..1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5741314"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

FEATURES
source
Query Match 59.4%; Score 869.2; DB 3; Length 1031;
ORIGIN

Best Local Similarity 95.9%; Pred. No. 9.5e-241; Matches 956; Conservative 0; Mismatches 34; Indels 7; Gaps 6;		CF785931		839 bp mRNA linear EST 20-OCT-2003	
Qy		31		AGENCOURT.15989463 NIH_MGC.220 Homo sapiens cDNA clone	
Db		1		IMAGE:30707295 5', mRNA sequence.	
Qy		91		AGTTGGGAGATTGGATATCGAATCCAGACCTGTCTTCTGACTATCTTCTTCAC	
Db		61		AGTTGGGAGATTGGATATCGAATCCAGACCTGTCTTCTGACTATCTTCTTCAC	
Qy		151		AGCTCTTCAGATCAATATGCTCCATCTGTTGGAGTATGACTGTTCCCAAGACCTT	
Db		121		AGCTCTTCAGATCAATATGCTCCATCTGTTGGAGTATGACTGTTCCCAAGACCT	
Qy		211		TTGAACAACAGTGAAGTAAACCGTCTTGGAGAGTGGATCCCAATCTTCTGGCCGGGT	
Db		181		TTGAACAACAGTGAAGTAAACCGTCTTGGAGAGTGGATCCCAATCTTCTGGCCGGGT	
Qy		271		TTTTTGTCTGACCTATGCGAGCAGCCATCCAGATTTAATAATATTTTGGACAGCT	
Db		241		TTTTTGTCTGACCTATGCGAGCAGCCATCCAGATTTAATAATATTTTGGACAGCT	
Qy		331		AGCATTATTTAGACAGATACAGCAAAATCTGCCAGCTGGTGTAGAGAGCTAGCA	
Db		301		AGCATTATTTAGACAGATACAGCAAAATCTGCCAGCTGGTGTAGAGAGCTAGCA	
Qy		391		GGAGACATTTCTGGGAATATGTTAGATGATATAGATACCTCTTTATTGTGCAAGCT	
Db		361		GGAGACATTTCTGGGAATATGTTAGATGATATAGATACCTCTTTATTGTGCAAGCT	
Qy		451		GCCATCCATCGAGGAATTAATGCTGTATGAACTAGGTGGCCAGATCACTGTGCTTACGCC	
Db		421		GCCATCCATCGAGGAATTAATGCTGTATGAACTAGGTGGCCAGATCACTGTGCTTACGCC	
Qy		511		AAGGGATCAGTCGATATGAAGGATTTCTGGCCAAATGGTCTTTTCGAGGGATGGTTC	
Db		481		AAGGGATCAGTCGATATGAAGGATTTCTGGCCAAATGGTCTTTTCGAGGGATGGTTC	
Qy		571		CTGTCCAGCAAGCAATTTCTGTGTACCTCAATGGTTCGAGCAGATCTTGTAGTTTGA	
Db		541		CTGTCCAGCAAGCAATTTCTGTGTACCTCAATGGTTCGAGCAGATCTTGTAGTTTGA	
Qy		631		CTTACCGGGCAATTCAGAGCTTTCTTCTCATGTCGAGTCGGTCAATGAGAGTGAGACCA	
Db		601		CTTACCGGGCAATTCAGAGCTTTCTTCTCATGTCGAGTCGGTCAATGAGAGTGAGACCA	
Qy		691		GTTCACTGGTCTCTGCGCCAGCCGACTTCAGGACCAAGCCCATCATGGCTTCGGGC	
Db		661		GTTCACTGGTCTCTGCGCCAGCCGACTTCAGGACCAAGCCCATCATGGCTTCGGGC	
Qy		751		GACAGTAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	
Db		721		GACAGTAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	
Qy		810		GAAATTAACAGGAATTAAGGACCAAGGATCTACAGTCGAACTTCACTTTTATG-TTA	
Db		781		GAAATTAACAGGAATTAAGGACCAAGGATCTACAGTCGAACTTCACTTTTATG-TTA	
Qy		869		AGAGTTTGTGATGAATCTTCAAAACCAATATTTCTAAGTGAAGACCTATTAAGGAATTG	
Db		841		AGAGTTTGTGATGAATCTTCAAAACCAATATTTCTAAGTGAAGACCTATTAAGGAATTG	
Qy		929		TGAATTAATGAAG--AAAAGTGTCTTTCAGGGTAACTCTAACTTTTC-GGGACCCAGTCAAA	
Db		899		TTGATATTGAAGAAAAGGGGTTTCAGGGTTAACTCTTAACTTTTCGGGGACCAATTCGAA	
Qy		986		ACAAATTCATCCCTCCCATCTGCGCCAGATATGTGG 1022	
Db		959		AACATTTTCATCCCTCCCTCGTGGCCCNATAAATGTG 995	


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Db 186 CGAGGGATGGTCCCTGTGACAGCAAGCGATTCTTGTTTACCTCCAATGGTTGCAGCAGAT 245
QY 617 CCTTGAAGTTTGAACCTGACGGCAATCAGAGCTTCTCCTCATCGCAGTCGGTCAATG 676
Db 246 CCTTGAAGTTTGAACCTGACGGCAATCAGAGCTTCTCCTCATCGCAGTCGGTCAATG 305
QY 677 AGAGTGGAGACCAAGTTCACTGCTCTCTGCGCAAGCCGACCTTCAGGACCAAGGCCCAT 736
Db 306 AGAGTGGAGACCAAGTTCACTGCTCTCTGCGCAAGCCGACCTTCAGGACCAAGGCCCAT 365
QY 737 CATGGCTCTGGCGCAGTAGCAACACCAACCAACAGAGTGGCTGGAGATCGATT 796
Db 366 CATGGCTCTGGCGCAGTAGCAACACCAACCAACAGAGTGGCTGGAGATCGATT 425
QY 797 TGGCGCAGAAAAGAAAATAACAGGAATTAGGACCAAGAGTCTACACAGTGGAACTTCA 856
Db 426 TGGCGGAGAAAAGAAAATAACAGGAATTAGGACCAAGAGTCTACACAGTGGAACTTCA 485
QY 857 ACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACCAATAATCTTAAGTGGAAACCT 916
Db 486 ACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACCAATAATCTTAAGTGGAAACCT 545
QY 917 ATAAAGGAATTGTAATATGAGAAAAGGTGTTTCAGGTAACCTTAACCTTCGGGACC 976
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QY 977 CAGTGCAAAACAAATTTTCATCCCTCCCATGCTGCGCAGATATGCGGGTTGTCGCCCAGA 1036
Db 606 CAGTGCAAAACAAATTTTCATCCCTCCCATGCTGCGCAGATATGCGGGTTGTCGCCCAGA 665
QY 1037 CATGGCACCAGAGGATAGCTTGAAGTGGAGTCAATGTTGGTCCAGATTTACAAAGGTA 1096
Db 666 CATGGCACCAGAGGATAGCTTGAAGTGGAGTCAATGTTGGTCCAGATTTACAAAGGTT 725
QY 1097 ATGATTCATTGTTGGTGGCGCAGACAGTCAAGACGACGATGTTTCACTAAGAAAG 1156
Db 726 ATGATTCATTGTTGGTGGCGCAGACAGTCAAGACGATCAAA-CACCATGTTTCCACTAGAAATAGAAG 784
QY 1157 A 1157
Db 785 A 785

CR749448 3600 bp mRNA linear HTC 19-AUG-2004
Homo sapiens mRNA; cDNA DKFZp686L21135 (from clone DKFZp686L21135).
CR749448.1 GI:51476605
HTC.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.
1 (bases 1 to 3600)
The German cDNA Consortium
Direct Submission
Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
Human Genome Project. This clone (DKFZp686L21135) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686L21135
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
```

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FEATURES
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Location/Qualifiers
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/mol_type="mrna"
/db_xref="taxon:9606"
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/clone_lib="686 (synonym: hlccc3). Vector pSport1_Sfi; host
DH10B_sites SfiIA + SfiIB"
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fully spliced"
1..3600
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CDS
208..>606
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GRGLLTIVASSDHPDLITCLERASHLYLKEFY"

Query Match 45.4%; Score 665; DB 4; Length 3600;
Best Local Similarity 91.1%; Pred. No. 3.2e-181; Indels 73; Gaps 1;
Matches 748; Conservative 0; Mismatches 0;

QY 1 ATGACATCTAAGAATTTATCCCGGACCTACCCCAATCACACTGTTTGCAGAAAGACAAT 60
Db 253 ATGACATCTAAGAATTTATCCCGGACCTACCCCAATCACACTGTTTGCAGAAAGACAAT 312
QY 61 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCAG 120
Db 313 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCAG 372
QY 121 ACCTGTGCTTCGACTATCTCTCTCACCAGCTCTTCAGATCAATATATGTCCTCATCTGT 180
Db 373 ACCTGTGCTTCGACTATCTCTCTCACCAGCTCTTCAGATCAATATATGTCCTCATCTGT 432
QY 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTAACACAAGTGAAGTAAACCGTCCGCTTT 240
Db 433 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTAACACAAGTGAAGTAAACCGTCCGCTTT 492
QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCAGCCAT 300
Db 493 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCAGCCAT 552
QY 301 CCAGATTTTAATAACATGTTTGGAAACGAGCTAGCCATTTTTCGAAGACAGATACAGCAAA 360
Db 553 CCAGATTTTAATAACATGTTTGGAAACGAGCTAGCCATTTTTCGAAGACAGATACAGCAAA 608
QY 361 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTTCTGGGAATATGGTAGTGA 420
Db 609 -----
QY 421 TATAGAGATACCTCTTTTATTGTGCAAGCTGCCATCCATGCAAGGAATAATTCGTATGAA 480
Db 609 -----ACCTCTTTATTGTGCAAGCTGCCATCCATGCAAGGAATAATTCGTATGAA 659
QY 481 CTAGTGGCCAGATCAGTGTGCTTCAGGCGCAAGGGATCAGTCGATATCAAGGGATTCTG 540
Db 660 CTAGTGGCCAGATCAGTGTGCTTCAGGCGCAAGGGATCAGTCGATATCAAGGGATTCTG 719
QY 541 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGTCAGACAGCGAATTTCTGTTTACCTCC 600
Db 720 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGTCAGACAGCGAATTTCTGTTTACCTCC 779
QY 601 AATGTTGACAGAGATCTTGTGATTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCCTCA 660
Db 780 AATGTTGACAGAGATCTTGTGATTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCCTCA 839
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/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/note="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p2), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 44.5%; Score 652; DB 7; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.2e-177; Indels 0; Gaps 0;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 358 AAATCTGCGCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGTTAGAT 417
DB 1 AAATCTGCGCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGTTAGAT 60
QY 418 GGNATAGAGATACCTCTTTATTTGTGGAAGCTGCCATCATCAGAGAAATAATTTGTGAT 477
DB 61 GGNATAGAGATACCTCTTTATTTGTGGAAGCTGCCATCATCAGAGAAATAATTTGTGAT 120
QY 478 GAACTAGGTGGCCAGATCAGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATT 537
DB 121 GAACTAGGTGGCCAGATCAGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATT 180
QY 538 CTGGCCAAATGTTGTTCTTTGAGGGATGTTCCCTGTGACAGCAAGCGATTTCGTGTTACC 597
DB 181 CTGGCCAAATGTTGTTCTTTGAGGGATGTTCCCTGTGACAGCAAGCGATTTCGTGTTACC 240
QY 598 TCAATGTTGACAGAGATCCTTTGAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCC 657
DB 241 TCAATGTTGACAGAGATCCTTTGAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCC 300
QY 658 TCATGCGAGTCCGTCAATGAGGTGAGACCAAGTTTCACTGCTCTCTCGCCAGGCCGA 717
DB 301 TCATGCGAGTCCGTCAATGAGGTGAGACCAAGTTTCACTGCTCTCTCGCCAGGCCGA 360
QY 718 CTTTCCAGCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACCA 777
DB 361 CTTTCCAGCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACCA 420
QY 778 GAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAAAATACAGGAATTAGGACCACAGA 837
DB 421 GAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAAAATACAGGAATTAGGACCACAGA 480
QY 838 TCTACACACTCGCACTTCACTTTATGTTTGAAGTTTGTGATGAATTCAGAAACAT 897
DB 481 TCTACACACTCGCACTTCACTTTATGTTTGAAGTTTGTGATGAATTCAGAAACAT 540
QY 898 AATTTCTAAGTGAAGACCTATAAGGAATTTGTAATTAATGAAGAAAGGTGTTTCAGGGT 957
DB 541 AATTTCTAAGTGAAGACCTATAAGGAATTTGTAATTAATGAAGAAAGGTGTTTCAGGGT 600
QY 958 AACTCTAACTTTCCGGACCCAGTCGCAAAACAATTTTCATCCCTCCCATCTGG 1009
DB 601 AACTCTAACTTTCCGGACCCAGTCGCAAAACAATTTTCATCCCTCCCATCTGG 652

RESULT 6

DN134443
LOCUS 866 bp mRNA linear EST 15-FEB-2005
DEFINITION 996566 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION DN134443
VERSION DN134443.1 GI:59828760
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus
1 (bases 1 to 866)
REFERENCE Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nouneman,D.J., Wray,J.E. and Keele,J.W.

TITLE
JOURNAL
COMMENT

Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: TMW8069 row: N column: 5
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

FEATURES

source

Query Match 34.6%; Score 506; DB 8; Length 866;
Best Local Similarity 84.5%; Pred. No. 3.5e-135;
Matches 598; Conservative 0; Mismatches 95; Indels 15; Gaps 2;
QY 768 CAAACACAGAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAAAATACAGGAATTAG 827
DB 9 CAAACAGAGAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAAAATACAGGAATTAG 68
QY 828 GACCAAGAGATCTACAGTCGAACTTCAACTTTTATGTTTAAAGAGTTTGTGATGAACCT 887
DB 69 GACCAAGAGATCCACAGTCGAACTTCAACTTTTACGTAAAGAGTTTGTGATGAACCT 128
QY 888 CAAACACATATTTCTAAGTGAAGACCTATAAGGAATTTGTAATTAAGAAAAAGT 947
DB 129 CAAAGCAATAGTCCAGTGGAGACTTATAAGGAATTTGGGAATTAATGAAGAAAAAGT 188
QY 948 GTTTCAGGGTAACTCTAACTTTCCGGACCCAGTCGCAAAACAATTTTCATCCCTCCCATCGT 1007
DB 189 GTTTCAGGGCACTCTAATTTTCGGGATCCCGTGGGAACAATCTTCCTCCCATTTGT 248
QY 1008 GGCACAGATATGTCGGGTTGTCCCCAGACATGGCCACAGAGATAGCCTTGAAGGTGA 1067
DB 249 GGCACAGATACATACGGTTTATCCCCATACCTGGCACAGAGATAGCCTTGAAGGTGA 308
QY 1068 GCTCATTTGTTGCCAGATTACA-----CAAGTAAATGATTCATTGTTGGGG 1115
DB 309 GCTTCTGGCTCCAGATTACACCAAGTAGGACTCAGGGTAAATGACTCATTGTTGGGC 368
QY 1116 CAAAGCAAGTCAAAAGCAGCAGTGTTCACCTAAGAAAGAGATGACACATCAAGAGCC 1175
DB 369 CAGACCAAGTTCAAATACCTGTTGGCTCAACTTAAGAGAGATGACACATCTCAACC 428
QY 1176 CATCCCTCCGGAAGAAACATCCACAGGAATAAACAATTACACGGTGGCTATTTCATTGTT 1235
DB 429 CATCCCTCTGAAGAAATGACCAAGGATTAACAACATCAACATCTGTTGTTATTCCACTG 488
QY 1236 GCTCTTGTGTTCTGGTGTGTTGCTGGAATGGGATCTTTGCGCCCTTTAGAAAGAGAA 1295
DB 489 GCTCC---TCGCCCTGCTGATTGCTGGAGTGGGAACCTTTTGCATCTTTAGAAAGAGAA 545
QY 1296 GAAAGAAAGAGAGTCCGTATGATGATCAGCGAGGCTCAGAAAAACAGACTGTTGGAAGCAGAT 1355
DB 546 GAAAGAAAGAGAGTCCGTATGATGATCAGCTAAGACTCAGAAAAACAGATTGTTGGAAGCAGAT 605
QY 1356 TAAATATCCCTTTGGCCAGACATCAGTCAGCTGAGTTTACCATCAGCTATGATAATGAGAA 1415

Db 606 CAAATATCCCTTTGCCAGGATCATGTCAGTGTAGTTTACATCATGTCAGTACATCATGAAAA 665

Qy 1416 GGAGATGACACAAAAGTTAGATCTCATCAAAAGTATGCGCAGTTA 1463

Db 666 GGAGATGACACAAAAGTTGGATCTCATCAAAAGTATGCGCAGTTA 713

RESULT 7

CD109068 913 bp mRNA linear EST 15-MAY-2003

LOCUS AGENCOURT 14020178 NIH_MGC_179 Homo sapiens cDNA clone

DEFINITION IMAGE:30367004 5', mRNA sequence.

ACCESSION CD109068

VERSION CD109068.1 GI:30762242

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 913)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: NDAM427 row: h column: 21
High quality sequence start: 15
High quality sequence stop: 652.

FEATURES

source Location/Qualifiers

1..913

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30367004"

/tissue_type="Pituitary"

/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"

/clone_lib="NIH_MGC_179"

/notes="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 33.4%; Score 489.6; DB 6; Length 913;

Best Local Similarity 95.5%; Pred. No. 2.1e-130;

Matches 569; Conservative 0; Mismatches 19; Indels 8; Gaps 6;

Qy 1 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAAATT 60

Db 299 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAAATT 358

Qy 61 ACAGTACAAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 120

Db 359 ACAGTACAAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 418

Qy 121 ACTGTGCTTCTGACTCTCTCTTCCACAGCTCTTCAGATCAATATGTCCTACTCTG 180

Db 419 ACTGTGCTTCTGACTCTCTCTTCCACAGCTCTTCAGATCAATATGTCCTACTCTG 478

Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 240

Db 479 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 538

Qy 241 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTTTGTGCTGACCTATGCGAGCAGCGACCAT 300

Db 539 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTTTGTGCTGACCTATGCGAGCAGCGACCAT 598

Qy 301 CCAGATTTTAAATAACATGTTTGGAAACGAGCTAGCCATTATTTCGAAGACAGAAATACAGCAA 360

Db 599 CCAGATTTTAAATAACGTTTGGAAACGAGCTAGCCATTATTTCGAAGACAGAAATACAGCAA 658

Qy 361 TTCTGCCACGCTGTTGTAGACAGCTAGCA-CGAGACATTTCTGGGAATATGTTAGATGG 419

Db 659 TTCTGCCACGCTGTTGTAGACAGCTAAACAGGAGACATTTCTGGGAATATGTTAGATGG 718

Qy 420 ATATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCGAGGATTAATTG-CTGATG 478

Db 719 ATATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCGAGGATTAATTGCTGATG 778

Qy 479 AACTA-GTGTGGCCAGATCAGT-GTGCTTCAGCGCAAGAGGATCAGTCGATATGAAGGGAT 536

Db 779 AACTANGTGTGGCAGATCATTTGTGCTTCGCCCAAAAGATCAGTCATATGAAGGGAT 838

Qy 537 TCTGGCCAAATGG-TGTTCTTTTCGAGGATGG--TTCCCTGTCAGACAAAGCGATTT 588

Db 839 TCTGGCCAAAGGTGTCCTTTCAAGGGAAGGGTTCCTCTGGTCAAAACAAGCGAATT 894

RESULT 8

CB988462 770 bp mRNA linear EST 01-MAY-2003

LOCUS AGENCOURT 13903537 NIH_MGC_147 Homo sapiens cDNA clone

DEFINITION IMAGE:30342255 5', mRNA sequence.

ACCESSION CB988462

VERSION CB988462.1 GI:30282982

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 770)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hanson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: NDAM375 row: a column: 16
High quality sequence stop: 607.

FEATURES

source Location/Qualifiers

1..770

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30342255"

/tissue_type="Human Placenta"

/lab_host="DH10B Tona"

/clone_lib="NIH_MGC_147"

/notes="Organ: placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamHI; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

ORIGIN

with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI, 3' end: BamHI. Host: DH10B.

FEATURES

source

1. .2835
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 /db_xref="taxon:10090"
 /clone="4631413K11"
 /tissue_type="skin"
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 74. .1456

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 /db_xref="GI:12852431"

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2816. .2821

polya_site

/note="putative"

ORIGIN

Query Match 30.8%; Score 451.4; DB 4; Length 2835;
 Best Local Similarity 84.1%; Pred. No. 3.7e-119;
 Matches 509; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAATTATCCCGGAGCTACCCCAATCACACTGTTTGGCAAGAACAAT 60
 DB 74 ATGACATCTAAGAATTATCAGGAGCTTACCCCAATTACACTGTGTGAAAGATCATC 133
 QY 61 ACAGTACCAAGGGGAAAGACTGATCTGAGTTGGGAGATTTGGATATCGAATCCGAG 120
 DB 134 ACAGTCCCAAGGGGAAAGAGACTTATCTGAGTTGGGAGATTTGAACATTTGAGTCCAAG 193
 QY 121 ACCGTGCTTCTGACTATCTCTTCCACCAGCTCTTCAGATCAATATGTCCTCACTGT 180
 DB 194 ACTGCGCTTCTGACTATCTCTTCCAGGATGCAACAGATCAGTATGTCCTCATATGT 253
 QY 181 GGAAGTATGACTGTCTCCCAAGAACTCTTGTGGAACAAGTGAAGTACCGTCCGCTTT 240
 DB 254 GCGAGTTGGCTGTTCCCAAGAACTCCCGTGAAGTCAAGCAAGTGAAGTCTCTCTTC 313
 QY 241 GAGAGTGGATCCACATTTCTGCGCGGGTCTTTCTGCTACCTATCGGAGCGAGCCAT 300
 DB 314 AAGAGTGGATCTCACATTTCTGCGCGGGCTTTCTGCTGACCTTACCGCAGAGTGACCAT 373
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 DB 374 CCAGATTTAATACCTGTTTGGAAACGAGCGAGCCATTATTTGAGGAAATAACACAAA 433
 QY 361 TTCTGCGCGAGCTGGTGTGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
 DB 434 TTCTGCGCGAGCTGGTGTGAGACATAGCAGGAGATTTCTGGGAATACAAAGATGT 493
 QY 421 TATAGAGATACCTCTTTTATTTGCAAGCTGCCATCCATCGAGGAATAATTTGCTGATGA 480
 DB 494 TACAGAGATACCTCTTTTATTTGCAAGCTGCCATCCAGCGAGGATCATCACAGATGA 553

QY 481 CTAGTGGCCAGATCAGTGTCTTTCAGCGAAGGATCAGTCGATATGAAGGATCTCTG 540
 DB 554 CTAGTGGCCAGATCAGTGTCTTTCAGCGAAGGATCAGTCGATATGAAGGATCTCTG 613
 QY 541 GCCAATGGGTGTTCTTTCGAGGGATGTTCCCTCTCAGACAAGGATTTCTGTGTACCTCC 600
 DB 614 GCCAATGGGTGTTCTTTCGAGGGATGTTCTTTCGAGAAAGGATTTCTTTTACCAAC 673
 QY 601 AATGG 605
 DB 674 CCAGG 678

RESULT 11

BY713935

LOCUS

DEFINITION

MUSCULUS

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BY713935 956 bp mRNA linear EST 17-DEC-2002
 musculus cDNA clone 4631413K11 5', mRNA sequence.

BY713935 GI:27126105

EST.

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 956)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Otsu, R., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalow, S., Beisel, K. W., Blake, J. A., Brad, D., Bruscia, V.,

Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,

Cariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,

Numata, K., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,

Sulcano, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-research.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, Y.,

Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,

Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,

Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,

Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,

Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken,
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 Location/Qualifiers
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 /sex="mixed"
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 skin"
 /notes="Site 1: SalI; Site 2: BamHI; cDNA library was
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 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTCTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 100.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATCTTCGAGTTAATTAATTAATCCGCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda FLX I"

ORIGIN

Query Match 30.4%; Score 445; DB 5; Length 956;
 Best Local Similarity 83.5%; Pred. No. 2e-117;
 Matches 505; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
 Qy 1 ATGACATCTAAGATTATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT 60
 Db 69 ATGACATCTAAGATTATCCAGGACTTACCCCAATTACACTGTGTGTTGAAAGATCATC 128
 Qy 61 ACAGTACAAAGGGGAAAGACTGATTCTGAGGTTGGAGATTGGATATCGAATCCAG 120
 Db 129 ACAGTCCAAAGGGGAAAGAGACTTATTCTGAGGTTGGAGATTGGAACATTTGAGTCCAAG 188
 Qy 121 ACCGTGCTCTGACTATCTTCTTCTTCCAGAGCTCTTCAGATCAATATGGTCCACTGT 180
 Db 189 ACCGTGCTCTGACTATCTTCTTCTTCCAGAGTGAACAGATCAGTATGTTCCATATGT 248
 Qy 181 GGAAGTATGACTGTTTCCAAAGAACTCTTGTGAAACAAAGTGAAGTAAACGTCGCTTT 240
 Db 249 GGGAGTTGGGCTGTTTCCAAAGAACTCGGGCTGAACCTCAAACGAGTGAAGTCTCTTTC 308
 Qy 241 GAGAGTGGATCCCACTTTCTGGCGGGGGTTTTTGTGCTATGCGAGCGAGGACCAT 300

Db 309 AAGAGTGGATCTCACATTTCTGGCGGGGCTTTCTGCTGACCTACGCCAGCAGTGACCAT 368
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 Db 369 CCAGATTTAATAACCTGTTTGGAAAGAGCGAGCCATTATTTTCGAGGAAAAATACAGCAA 428
 Qy 361 TTCTGCCAGCTGGTGTAGAGACGTAGCAGAGACATTTCTGGGGAATATGGTAGATGGA 420
 Db 429 TTCTGCCAGCTGGCTGTAGAGACATAGCAGGAGATATTTCTGGGGAATACAAAAGATGGT 488
 Qy 421 TATAGAGATACCTCTTATTTGCAAGCTGCCATCCATGCGAGGATATTTCTGATGAA 480
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 Qy 541 GCAATGGTGTCTTTCTGAGGAGATGTTCCCTGTCAGACAAAGGATTTCTGTTTACCTCC 600
 Db 609 GTCAATGGGCTGCTCTCCGCGCATGTTCTTTGTGCGAAGAGCGATTCTCTTTTACAACC 668
 Qy 601 AATGG 605
 Db 669 CCAGG 673
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 LOCUS RC4-ST0185-131099-011-c01 ST0185 Homo sapiens cDNA, mRNA EST 04-FEB-2000
 DEFINITION AM390343
 ACCESSION AM390343
 VERSION AM390343.1 GI:6895002
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 466)
 HGCP <http://www.ludwig.org.br/ORESTES>.
 AUTHORS The FAPESP/LICR Human Cancer Genome Project
 TITLE Unpublished (1999)
 JOURNAL Contact: Simpson A.J.G.
 COMMENT Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-ST0185-131099-011-c01&t3=1999-10-13&t4=i1>)
 Seq primer: puc 18 forward
 High quality sequence start: 26
 High quality sequence stop: 204.
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 /dev_stage="Adult"
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 /note="Organ: stomach; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

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Query Match      29.7%; Score 434.2; DB 1; Length 466;
Best Local Similarity 97.0%; Pred. No. 2.2e-114;
Matches 453; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 512 AAGGGATCAGTCGATGAGGAGTCTGGCCCAATGGTGTCTTTTCGAGGAGTGGTCCC 571
DB 466 AAGGGATCAGTCGATGAGGAGTCTGGCCCAATGGTGTCTTTTCGAGGAGTGGTCCC 407

QY 572 TGTTCACAGAGCGATTTCTGTCTTACCTCCATGCTGGTGCAGCAGATCTTGGATTTGAAC 631
DB 406 TGTTCACAGAGCGATTTCTGTCTTACCTCCATGCTGGTGCAGCAGATCTTGGATTTGAAC 347

QY 632 CTGACGGGCAAAATCAGAGCTTCTTCTCATGGCAGTCCGTCATGAGAGTGGAGACCAAG 691
DB 346 CTGACGGGCAAAATCAGAGCTTCTTCTCTTGGCAGTCCGTCATGAGTGGAGACCAAG 287

QY 692 TTCACCTGGTCTCTGCGCCAAAGCCGACTTCAGGACCAAGGCCCATCATGGGCTTCGGGCG 751
DB 286 TTCACCTGGTCTCTGCGCCAAAGCCGACTTCAGGACCAAGGCCCATCATGGGCTTCGGGCG 227

QY 752 ACAGTAGCACACACCAACCAACGAGAGTGGCTGAGATCGATTTGGGGGAGAAAAAGA 811
DB 226 ACAGTAGCACACACCAACCAACGAGAGTGGCTGAGATCGATTTGGGGGAGAAAAAGA 167

QY 812 AAATAACAGGAATTAGGACACACAGGATCTACACAGTCCGAACCTTCAACTTTTATGTTAAGA 871
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QY 872 GTTTTGTGATGAATTTCAAAAAAATAATTTCTAAGTGGAGAGCCTATAAGGAATTTGTA 931
DB 106 GTTTTGTGATGAATTTCAAAAAAATAATTTCTAAGTGGAGAGCCTATAAGGAATTTGTA 47

QY 932 ATAATCAAGAAAGGTGTTTCAGGTTAACTTCAACTTTCCGGACCCA 978
DB 46 ATAATCAAGAAAGGTGTTTCAGGTTAACTTCAACTTTCCGGACCCA 1
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RESULT 13

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BX360287 Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 683)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30376427.
```

REFERENCE

```
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3863.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?S=CSODI067DG100P1&c=3863.f.
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FEATURES

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source
Location/Qualifiers
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ORIGIN

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Matches 428; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 121 ACTGTGCTTCTGACATATCTTCTTTCACAGCTCTTTCAGATCAATATGTTCCATCTGT 180
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QY 181 GGAAGTATGACATGTTTCCCAAGAACTCTTTGTTGAACACAAAGTAAACCGTCCGCTTT 240
DB 435 GGAAGTATGACATGTTTCCCAAGAACTCTTTGTTGAACACAAAGTAAACCGTCCGCTTT 494

QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTCTGCTGACCTATTCGAGCAGCGACCAT 300
DB 495 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTCTGCTGACCTATTCGAGCAGCGACCAT 554

QY 301 CCAGATTTAATAACATGTTTGGAAACAGCTAGCCATATTTGAAGACAGAAATACAGCAA 360
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QY 361 TTCTGCGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGAAATATGGTAGTGA 420
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QY 421 TATAGAGAT 429
DB 675 TATAGAGAT 683
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RESULT 14

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BX345014
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 686)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30342328.
```

REFERENCE

```
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
```

division of Invitrogen. This sequence belongs to sequence cluster 3863.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS2BAX14ZH08_AX24ZE2_1&c=3863.f.

FEATURES

source
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 29.0%; Score 424.2; DB 5; Length 686;
Best Local Similarity 99.3%; Pred. No. 2e-111;
Matches 426; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 121 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGTCCTACTACTGT 180
DB 378 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGTCCTACTACTGT 437
QY 181 GGAAGTATGACTGTTCCCAAGAGACTCTTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 240
DB 438 GGAAGTATGACTGTTCCCAAGAGACTCTTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 497
QY 241 GAGAGTGGATCCCAATCTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 300
DB 498 GAGAGTGGATCCCAATCTTCTGCGCGAGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 557
QY 301 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATTAATTTGAAGACAGAAATACAGAAA 360
DB 558 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATTAATTTGAAGACAGAAATACAGAAA 617
QY 361 TTCTGCCCGAGCTGTTGAGAGAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
DB 618 TTCTGCCCGAGCTGTTGAGAGAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 677
QY 421 TATAGAGAT 429
DB 678 TATAGAGAT 686

RESULT 15

CB960471
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DEFINITION AGENCOURT 13887572 NIH MGC_147 Homo sapiens cDNA clone
IMAGE:30347405 5', mRNA sequence.

ACCESSION CB960471
VERSION CB960471.1 GI:30216587
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 798)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: NDAM388 row: h column: 06
High quality sequence stop: 707.

FEATURES

source

1. .798
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30347405"
/issue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Query Match 27.7%; Score 405.4; DB 6; Length 798;
Best Local Similarity 99.8%; Pred. No. 6e-106;
Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACAACCTGTTTCGGAAGACAAATT 60
DB 363 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACAACCTGTTTCGGAAGACAAATT 422
QY 61 ACAGTACCAAGGGGAAAGAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCGAG 120
DB 423 ACAGTACCAAGGGGAAAGAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCGAG 482
QY 121 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGTCCTACTACTGT 180
DB 483 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGTCCTACTACTGT 542
QY 181 GGAAGTATGACTGTTCCCAAGAGAACTCTTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 240
DB 543 GGAAGTATGACTGTTCCCAAGAGAACTCTTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 602
QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 300
DB 603 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 662
QY 301 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATTAATTTGAAGACAGAAATACAGAAA 360
DB 663 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATTAATTTGAAGACAGAAATACAGAAA 722
QY 361 TTCTGCCCGAGCTGTTGAGAGAGCTAGCAGGAGACATTTCTGGGAA 407
DB 723 TTCTGCCCGAGCTGTTGAGAGAGCTAGCAGGAGACATTTCTGGGGA 769

Search completed: January 15, 2006, 19:22:26

Job time : 5454 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:09:37 ; Search time 864 Seconds

(without alignments)

11292.951 Million cell updates/sec

Title: US-10-813-588-1

Perfect score: 1464

Sequence: 1 atgacatctaagaattatcc.....caagtgatatgcaggttaa 1464

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464	100.0	1620	4	AAS00615 Novel hum
2	1464	100.0	1761	4	AAS00614 Novel hum
3	1464	100.0	1768	4	AAS00613 Novel hum
4	1462.4	99.9	1761	11	ADN39765 Cancer/an
5	1462.4	99.9	2010	11	ADN39764 Cancer/an
6	1462.4	99.9	2010	13	ADR46610 Cancer-as
7	1462.4	99.9	2010	13	ADR46611 Cancer-as
8	1459.8	99.7	2145	8	ACD66718 Secreted
9	1459.8	99.7	2145	12	ADQ10135 Human pol
10	1459.8	99.7	2888	6	ADI28055 ECMCAD ge
11	1459.8	99.7	3151	6	ABN86493 Human neu
12	1459.8	99.7	3594	8	AAS00660 Human TAN
13	1459.8	99.7	3594	8	ACD66717 Secreted
14	1459.8	99.7	3594	12	ADQ10134 Human pol
15	1459.8	99.7	3676	5	ADL62155 Human ova
16	1440.2	98.4	2547	11	ADM02314 Human CUN
17	1107.4	75.6	2310	11	ADN39766 Cancer/an
18	1040.6	71.1	2145	6	ABN86496 Human zcu
19	584.2	39.9	2473	11	ADM03690 Human CUN

20	584.2	39.9	2473	14	ADV18582	Adv18582 DNA encod
21	565.6	38.6	636	8	ACA10146	ACA10146 Human NOV
22	564.2	38.5	1538	8	ACA10145	ACA10145 Human NOV
23	564.2	38.5	1538	12	ADO08322	ADO08322 Human NOV
24	563	38.5	636	12	ADO08324	ADO08324 Human NOV
25	556	38.0	1265	6	AAD35992	AAD35992 Human neu
26	556	38.0	1265	6	ABK49565	ABK49565 Human CDN
27	556	38.0	1265	10	ADC29936	ADC29936 Human nov
28	548	37.4	596	14	ADV74982	Adv74982 Human col
29	451.4	30.8	2836	6	ABN86494	ABN86494 Mouse zcu
30	449.8	30.7	1871	3	AAA96736	AAA96736 Polynucle
31	414.4	28.3	456	9	ACH31919	ACH31919 Human end
32	400	27.3	400	14	ADV74981	Adv74981 Human col
33	368.2	25.2	1509	6	ABN86497	ABN86497 Mouse zcu
34	223	15.2	2868	6	ABN86495	ABN86495 Mouse zcu
35	219.4	15.0	407	2	AAV87469	AAV87469 EST clone
36	205.8	14.1	2310	9	ADA00876	ADA00876 Mouse ESD
37	205.6	14.0	2020	10	ADA53293	ADA53293 Human cod
38	205.6	14.0	2046	3	AAZ51872	Aaz51872 Human Fac
39	205.6	14.0	6093	10	ADA19345	Ada19345 Human ins
40	205.6	14.0	6595	12	ADQ23685	Adq23685 Human sof
41	204	13.9	1962	8	ABX93043	Abx93043 Human LCC
42	204	13.9	2200	6	ABA00056	Abao00056 CADHP-3 c
43	204	13.9	2280	8	ABX93042	Abx93042 Human LCC
44	204	13.9	2328	9	ADA00874	Ada00874 Human ESD
45	204	13.9	2391	9	AAL62024	Aal62024 Human cel

ALIGNMENTS

RESULT 1

AAS00615

ID AAS00615 standard; cDNA; 1620 BP.

XX AAS00615;

XX 29-AUG-2001 (first entry)

DE Novel human protein (NHP) DNA sequence #3.

XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1620

FT /tag= a

FT /product= "Novel human protein #3"

XX WO200129219-A1.

XX 26-APR-2001.

XX 08-OCT-2000; 2000WO-US028798.

PR 19-OCT-1999; 99US-0160285P.

PR 18-FEB-2000; 2000US-0183583P.

PA (LEXI-) LEXICON GENETICS INC.

PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;

PI Sands AT;

DR WPI; 2001-290917/30.

XX P-PSDB; AAU00630.

XX Novel nucleic acid encoding human CUB-domain containing protein, useful
PT for drug screening, diagnosis and treatment of physiological disorders or
PT diseases.

Disclosure; Page 28-29; 33pp; English.

The sequence represents a polynucleotide which encodes a novel human protein (NHP) containing a CUB domain (an extracellular domain). CUB proteins have been associated with regulating development, modulating cellular processes and preventing infectious disease. NHP nucleotide sequences are useful for gene therapy of physiological disorders or diseases. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene patterns. NHP nucleotide sequences are useful for detecting mutant or inappropriately expressed NHPs (for example, those proteins associated with obesity, high blood pressure, connective tissue disorders and infertility) for the diagnosis of a disease. The polynucleotides may also be used in screening for drugs effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. Nucleotide constructs encoding NHP products are used to genetically engineer host cells to express such products *in vivo*. These host cells allow for the identification of compounds that bind to NHP receptors or trigger NHP-mediated pathways.

Sequence 1620 BP: 456 A: 353 C: 422 G: 389 T: 0 U: 0 Other:

every Match 100.0%; Score 1464; DB 4; Length 1620;

Best Local Similarity 100.0%; Pred. No. 0;

atches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACATCTAAGAAATTATCCGGGACCTTACCCCAATCACACTGTTTGGAAAGACAAATT 60
157 ATGACATCTAAGAAATTATCCGGGACCTTACCCCAATCACACTGTTTGGAAAGACAAATT 216
61 ACAGTACCAAAGGGGAAAGACTGATTCGAGGTTGGGAGATTGGATATCGAATCCCAAG 120
217 ACAGTACCAAAGGGGAAAGACTGATTCGAGGTTGGGAGATTGGATATCGAATCCCAAG 276
121 ACCTGTGCTTCGACTATCTCTCTTCACACGACTCTTCAGATCAATATGGTCCCACTGTT 180
277 ACCTGTGCTTCGACTATCTCTCTTCACACGACTCTTCAGATCAATATGGTCCCACTGTT 336
181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACAAGAGTGAAGTAACCGTCGGCTTT 240
337 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACAAGAGTGAAGTAACCGTCGGCTTT 396
241 GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTTCGCTGACCTATGCGAGCAGCGACAT 300
397 GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTTCGCTGACCTATGCGAGCAGCGACAT 456
301 CCAGATTTTAATAACATGTTTGGAAACGAGCTAGCCCAATTTATGGAACACAGAAATACAGCAA 360
457 CCAGATTTTAATAACATGTTTGGAAACGAGCTAGCCCAATTTATGGAACACAGAAATACAGCAA 516
361 TTCTGCCACGCTGGTTGTGAGACGCTAGCAGGAGACATTTCTGGGAAATATGTTAGATGGA 420
517 TTCTGCCACGCTGGTTGTGAGACGCTAGCAGGAGACATTTCTGGGAAATATGTTAGATGGA 576
421 TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCAAGGAATAATTTGCTGATGAA 480
577 TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCAAGGAATAATTTGCTGATGAA 636
481 CTAGGTGGCCAGATCAGTGTGCTTCAGGCCAAAGGGATCAGTCCGATATGAAGGGGATTCGT 540
637 CTAGGTGGCCAGATCAGTGTGCTTCAGGCCAAAGGGATCAGTCCGATATGAAGGGATTCGT 696
541 GCCAATGGTGTCTTTCGAGGGAATGGTTCCCTGTGCAGACAGCGAATTTCTGTTTACCTCC 600
697 GCCAATGGTGTCTTTCGAGGGAATGGTTCCCTGTGCAGACAGCGAATTTCTGTTTACCTCC 756
601 AATGGTTGCAGCAGATCCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCCCTCA 660
757 AATGGTTGCAGCAGATCCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCCCTCA 816
661 TGGCAGTCCGCTCAATGAGAGTGGAGCCAAAGTTCACTGGTCTCTCGGCCAAGCCCGACTT 720
817 TGGCAGTCCGCTCAATGAGAGTGGAGCCAAAGTTCACTGGTCTCTCGGCCAAGCCCGACTT 876

Db 1139 CAGATTACACAAGTAATGATTCATTGGTGTGGCGCAAGACAAAGTCAAAGCCAGCGTT 1198
Qy 1141 TCAACTAAGAAGAGATGAGACAATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1199 TCAACTAAGAAGAGATGAGACAATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1258
Qy 1201 GGAATAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTGTCTGGTGTGCT 1260
Db 1259 GGAATAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTGTCTGGTGTGCT 1318
Qy 1261 GGAATGGGATCTTTGAGAGCTTTAGAAAGAGAGAAAGAAAGTCCGTATGATCA 1320
Db 1319 GGAATGGGATCTTTGAGAGCTTTAGAAAGAGAGAAAGAAAGTCCGTATGATCA 1378
Qy 1321 GCGAGGCTCAGAAAACAGACTGTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
Db 1379 GCGAGGCTCAGAAAACAGACTGTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1438
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1439 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAAGTTAGATCTC 1498
Qy 1441 ATCACAAGTCATATGGCAGGTTAA 1464
Db 1499 ATCACAAGTCATATGGCAGGTTAA 1522

RESULT 4

ADN39765

ID ADN39765 standard; cDNA; 1761 BP.

AC ADN39765;

XX

ADN39765 (first entry)

DT 17-JUN-2004

XX Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO: C137.

DE Human;

XX Human; differential expression; cancer; angiogenic disorder;

KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

KW inflammatory disease; autoimmune disease;

KW retinal neovascularisation syndrome; scarring; uterine fibroid;

KW detection; diagnosis; prognosis; drug screening; drug targeting;

KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;

KW vulnery; gene therapy; vaccine; gene; ss.

XX Homo sapiens.

OS

XX WO2003042661-A2.

PN

XX 22-MAY-2003.

PD

XX 13-NOV-2002; 2002WO-US036810.

PF

XX 13-NOV-2001; 2001US-0350666P.

XX 21-NOV-2001; 2001US-0332464P.

PR 29-NOV-2001; 2001US-0334393P.

PR 03-DEC-2001; 2001US-0335394P.

PR 14-DEC-2001; 2001US-0340376P.

PR 08-JAN-2002; 2002US-0347211P.

PR 08-FEB-2002; 2002US-0347349P.

PR 10-FEB-2002; 2002US-0355250P.

PR 13-FEB-2002; 2002US-0356714P.

PR 20-FEB-2002; 2002US-0359077P.

PR 29-MAR-2002; 2002US-0368809P.

PR 04-APR-2002; 2002US-0370110P.

PR 12-APR-2002; 2002US-0372246P.

PR 05-JUN-2002; 2002US-0386614P.

PR 16-JUL-2002; 2002US-0396839P.

PR 22-JUL-2002; 2002US-0397759P.

PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.

XX (E0SB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
DR P-PSDB; ADN39982.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.

XX Claim 8; SEQ ID NO C137; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.

XX Sequence 1761 BP; 472 A; 402 C; 482 G; 405 T; 0 U; 0 Other;

Query Match 99.9%; Score 1462.4; DB 11; Length 1761;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTGTTTGCAGAAAGACAATT 60

Db 298 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTGTTTGCAGAAAGACAATT 357

Qy 61 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 120

Db 358 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 417

Qy 121 ACCTGTGCTTCTGACTATCTTCTTCCAGCAGCTTTCAGATCAATATGGTCCATACTGT 180

Db 418 ACCTGTGCTTCTGACTATCTTCTTCCAGCAGCTTTCAGATCAATATGGTCCATACTGT 477

Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACACAAAGTGAAGTAAACCGTCCGCTTT 240

Db 478 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACACAAAGTGAAGTAAACCGTCCGCTTT 537

Qy 241 GAGAGTGGATCCACATTTCTGCGGGGGTTTTTCTGACCTATCGGAGCAGCGACCAT 300

Db 538 GAGAGTGGATCCACATTTCTGCGGGGGTTTTTCTGACCTATCGGAGCAGCGACCAT 597

Qy 301 CCAGATTTAATAACATGTTTGGACAGCTAGCCATTTTGGAGACAGNATACAGCAAA 360

Db 598 CCAGATTTAATAACATGTTTGGACAGCTAGCCATTTTGGAGACAGNATACAGCAAA 657

Qy 361 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420

Db 658 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 717

Qy 421 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTGCTGATGA 480

Db 718 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTGCTGATGA 777

Qy 481 CTAGTGGCCAGATCAGTGTGCTTACGCGAAAGGATCAGTCGATATGAGGAGATCTG 540

Db 778 CTAGTGGCCAGATCAGTGTGCTTACGCGAAAGGATCAGTCGATATGAGGAGATCTG 837

Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGCGAAGAGACAATT	60
DB	282	ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGCGAAGAGACAATT	341
QY	61	ACAGTACCAAAGGGGAAAGATGATTTCTGAGGTGGGAGATTTGGATATCGAATCCAG	120
DB	342	ACAGTACCAAAGGGGAAAGATGATTTCTGAGGTGGGAGATTTGGATATCGAATCCAG	401
QY	121	ACCTGTGCTTCTGACTATCTTCTTCCACCAGCTCTTCAGATCAATATGGTCAATCTGT	180
DB	402	ACCTGTGCTTCTGACTATCTTCTTCCACCAGCTCTTCAGATCAATATGGTCAATCTGT	461
QY	181	GGAGTATGACTGTTCCCAAGAACTCTTGTTCGAACACAGTGAAGTAAACCGTCCGCTTT	240
DB	462	GGAGTATGACTGTTCCCAAGAACTCTTGTTCGAACACAGTGAAGTAAACCGTCCGCTTT	521
QY	241	GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTGTCTGACCTATTCGAGCAGCGACCAT	300
DB	522	GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTGTCTGACCTATTCGAGCAGCGACCAT	581
QY	301	CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTTGAAGACAGATACAGCAAA	360
DB	582	CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTTGAAGACAGATACAGCAAA	641
QY	361	TTCTGCCAGCTGTTGTAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA	420
DB	642	TTCTGCCAGCTGTTGTAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA	701
QY	421	TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTTGCTGATGA	480
DB	702	TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTTGCTGATGA	761
QY	481	CTAGTGGCCAGATCAGTGTCTTTCAGCGAAGGGATCAGTCGATATGAAGGATCTTG	540
DB	762	CTAGTGGCCAGATCAGTGTCTTTCAGCGAAGGGATCAGTCGATATGAAGGATCTTG	821
QY	541	GCCAATGGTGTCTTTTCGAGGAGTGTTCCTGTGACAGCGATTTCTGTTTACTCTCC	600
DB	822	GCCAATGGTGTCTTTTCGAGGAGTGTTCCTGTGACAGCGATTTCTGTTTACTCTCC	881
QY	601	AATGTTTGACAGATCTTGTAGTGTGTTGAACCTGACGGCAATTCAGAGCTTCTTCTCA	660
DB	882	AATGTTTGACAGATCTTGTAGTGTGTTGAACCTGACGGCAATTCAGAGCTTCTTCTCA	941
QY	661	TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCACTGCTCTGCGCAAGCCGACTT	720
DB	942	TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCACTGCTCTGCGCAAGCCGACTT	1001
QY	721	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACACCAACACGAGAG	780
DB	1002	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACACCAACACGAGAG	1061
QY	781	TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGATCT	840
DB	1062	TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGATCT	1121
QY	841	ACAGTGGAACTTCAACTTTTATGTTAAGAGTGTGATGAATTTCAAAACCAATAAT	900
DB	1122	ACAGTGGAACTTCAACTTTTATGTTAAGAGTGTGATGAATTTCAAAACCAATAAT	1181
QY	901	TCTAAGTGAAGACCTATTAAGGAATTGTGAATAATGAAGAAAGTGTTCAGGGTAA	960
DB	1182	TCTAAGTGAAGACCTATTAAGGAATTGTGAATAATGAAGAAAGTGTTCAGGGTAA	1241
QY	961	TCTAACTTTCCGAGCCAGTGCAGAAACAATTTTATCCCTCCCATCGTGGCCAGATATG	1020
DB	1242	TCTAACTTTCCGAGCCAGTGCAGAAACAATTTTATCCCTCCCATCGTGGCCAGATATG	1301
QY	1021	CGGGTTGCCCCAGACATGGCACGAGGATAGCCCTGAAGGTGAGCTCATTTGGTTGC	1080
DB	1302	CGGGTTGCCCCAGACATGGCACGAGGATAGCCCTGAAGGTGAGCTCATTTGGTTGC	1361

QY	1081	CAGATTACACAAGGTAATGATTCATTTGGTGTGCGCAAGACAGTCAAAAGCACCAGTGT	1140
DB	1362	CAGATTACACAAGGTAATGATTCATTTGGTGTGCGCAAGACAGTCAAAAGCACCAGTGT	1421
QY	1141	TCAACTAAGAAAGAGATGAGACAATTCACAAGGCCCATCCCTCGGAAGAAACATCCACA	1200
DB	1422	TCAACTAAGAAAGAGATGAGACAATTCACAAGGCCCATCCCTCGGAAGAAACATCCACA	1481
QY	1201	GGAAATAAACATTTACAACGGTGGCTATTCCATTGGTGTCTCTGTTGTTCTGTTGCT	1260
DB	1482	GGAAATAAACATTTACAACGGTGGCTATTCCATTGGTGTCTCTGTTGTTCTGTTGCT	1541
QY	1261	GGAAATGGGATCTTTTGCAGCCCTTGAAGAAAGAAAGAAAGAAAGTCCGTATGATCA	1320
DB	1542	GGAAATGGGATCTTTTGCAGCCCTTGAAGAAAGAAAGAAAGAAAGTCCGTATGATCA	1601
QY	1321	GCGGAGGCTCAGAAAAACAGACTGTTGGAAAGCAGATTTAAATATCCCTTTGCCAGACATCAG	1380
DB	1602	GCGGAGGCTCAGAAAAACAGACTGTTGGAAAGCAGATTTAAATATCCCTTTGCCAGACATCAG	1661
QY	1381	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC	1440
DB	1662	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC	1721
QY	1441	ATCACAAAGTGATATGSCAGGTTAA	1464
DB	1722	ATCACAAAGTGATATGSCAGGTTAA	1745
RESULT 6			
ADR46610			
ID	ADR46610	standard; DNA; 2010 BP.	
XX	AC	ADR46610;	
XX	DT	18-NOV-2004 (first entry)	
DE	XX	Cancer-associated protein coding sequence, SEQ ID 23.	
XX	XX	Cytostatic; Gene Therapy; cancer; human; gene; ds.	
OS	XX	Homo sapiens.	
EH	XX	Location/Qualifiers	
FT	XX	126..1745	
FT	XX	/*tag= a	
XX	XX	/product= "Cancer-associated protein, SEQ ID 81"	
PN	XX	WO2004073657-A2.	
PD	XX	02-SEP-2004.	
PF	XX	19-FEB-2004; 2004WO-US005455.	
PR	XX	19-FEB-2003; 2003US-0448784P.	
PA	XX	(PROT-) PROTEIN DESIGN LABS INC.	
PI	XX	Aziz N, Gish KC, Wilson KE, Zlotnik A;	
DR	XX	WPI; 2004-652787/63.	
XX	XX	P-PSDB; ADR46668.	
PT	XX	Detecting a pathological cell in a patient for diagnosing or treating	
PT	XX	cancer by detecting in a biological sample from the patient genes whose	
PT	XX	-expression are up-regulated or down-regulated in specific cancers.	
PS	XX	Claim 1; SEQ ID NO 23; 375pp; English.	
CC	XX	The present invention relates to a method for detecting cancer in a	
CC	XX	patient. The method comprises detecting in a biological sample from the	
CC	XX	patient a nucleotide or protein sequence comprising a sequence that is at	

CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
CC cancer for preparing a composition for diagnosing or treating cancer.
XX
SQ Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;

Query Match 99.9%; Score 1462.4; DB 13; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCAGACTGTTTGGGAAAGACAATT 60
DB 282 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCAGACTGTTTGGGAAAGACAATT 341

QY 61 ACAGTACCAAGGGGAAAGACTGATTCTGAGGTGGGAGATTGGATATCGAATCCCGAG 120
DB 342 ACAGTACCAAGGGGAAAGACTGATTCTGAGGTGGGAGATTGGATATCGAATCCCGAG 401

QY 121 ACCTGTGCTTCTGACTATCTTCTCTTCCACGAGCTTTCAGATCAATATGTCCTACTGT 180
DB 402 ACCTGTGCTTCTGACTATCTTCTCTTCCACGAGCTTTCAGATCAATATGTCCTACTGT 461

QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAGAGTGAAGTAAACCGTCCGCTTT 240
DB 462 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAGAGTGAAGTAAACCGTCCGCTTT 521

QY 241 GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTGTGACCTATGCGAGCAGACCAT 300
DB 522 GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTGTGACCTATGCGAGCAGACCAT 581

QY 301 CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTATGAAGACAGAAATACAGAAA 360
DB 582 CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTATGAAGACAGAAATACAGAAA 641

QY 361 TTCTGCCAGCTGTTAGAGAGTGAAGAGACATTTCTGGGAATATGTTAGATGA 420
DB 642 TTCTGCCAGCTGTTAGAGAGTGAAGAGACATTTCTGGGAATATGTTAGATGA 701

QY 421 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCCTATGAGGAATATTTGCTGATGA 480
DB 702 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCCTATGAGGAATATTTGCTGATGA 761

QY 481 CTAGGTGGCCAGATCAGTGTCTTTGAGCGAAAGGATCAGTGCATATGAAGGATCTG 540
DB 762 CTAGGTGGCCAGATCAGTGTCTTTGAGCGAAAGGATCAGTGCATATGAAGGATCTG 821

QY 541 GCCAATGGTGTCTTTGAGGGATGGTTCCTGTGAGCAAGCGATTTCTGTTTACCTCC 600
DB 822 GCCAATGGTGTCTTTGAGGGATGGTTCCTGTGAGCAAGCGATTTCTGTTTACCTCC 881

QY 601 AATGGTTGACGAGATCCTTGTGATTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 660
DB 882 AATGGTTGACGAGATCCTTGTGATTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 941

QY 661 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGGCCAAAGCCGACTT 720
DB 942 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGGCCAAAGCCGACTT 1001

QY 721 CAGGACCAAGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 780
DB 1002 CAGGACCAAGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 1061

QY 781 TGGCTGGAGATCGATTTTGGGGGAGAAAAGAAAATAACAGGAATTTAGGACCAAGGATCT 840
DB 1062 TGGCTGGAGATCGATTTTGGGGGAGAAAAGAAAATAACAGGAATTTAGGACCAAGGATCT 1121

QY 841 ACACAGTGGAACTTCAACTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 900
DB 1122 ACACAGTGGAACTTCAACTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1181

QY 901 TCTAAGTGGAGACCTTAAAGGAATTTGTAATATGAAGAAAGGTTTTCAGGGTAAAC 960
DB 1182 TCTAAGTGGAGACCTTAAAGGAATTTGTAATATGAAGAAAGGTTTTCAGGGTAAAC 1241

QY 961 TCTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCTCCCTCCATCGTGGCCAGATATGTG 1020
DB 1242 TCTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCTCCCTCCATCGTGGCCAGATATGTG 1301

QY 1021 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCTTTGAAGGTGGAGCTCAATGGTTGC 1080
DB 1302 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCTTTGAAGGTGGAGCTCAATGGTTGC 1361

QY 1081 CAGATTACACAAGGTAATGATTTCAATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCAGTGT 1140
DB 1362 CAGATTACACAAGGTAATGATTTCAATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCAGTGT 1421

QY 1141 TCAACTAAGAAAAGAGATGAGACAATCACAAGGCCCATCTCCCTCGGAAGAAACATCCACA 1200
DB 1422 TCAACTAAGAAAAGAGATGAGACAATCACAAGGCCCATCTCCCTCGGAAGAAACATCCACA 1481

QY 1201 GGAATTAACATTTACACGGTGGCTATTCATTTGGTGTCTCTTGTCTCTGGTGTGTGCT 1260
DB 1482 GGAATTAACATTTACACGGTGGCTATTCATTTGGTGTCTCTTGTCTCTGGTGTGTGCT 1541

QY 1261 GGAATGGGATCTTTTCAGCCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
DB 1542 GGAATGGGATCTTTTCAGCCCTTTAGAAAAGAAAGAAAGTCCGTATGATCA 1601

QY 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAAGCAGATTAAATATATCCCTTGGCCAGACATCAG 1380
DB 1602 GCGAGGCTCAGAAAACAGACTGTTGGAAAGCAGATTAAATATATCCCTTGGCCAGACATCAG 1661

QY 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAAGAGGAGATGACACAAAAGTTAGATCTC 1440
DB 1662 TCAGCTGAGTTTACCATCAGCTATGATATGAAGAGGAGATGACACAAAAGTTAGATCTC 1721

QY 1441 ATCACAAGTGATATGGCAGTTAA 1464
DB 1722 ATCACAAGTGATATGGCAGTTAA 1745

RESULT 7
ADR46611
ID ADR46611 standard; DNA; 2010 BP.
XX ADR46611;
XX AC ADR46611;
XX DT 18-NOV-2004 (first entry)
XX DE Cancer-associated protein coding sequence, SEQ ID 24.
XX KW Cytostatic; Gene Therapy; cancer; human; gene; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 126..1745
XX FT /*tag= a
XX FT /product= "Cancer-associated protein, SEQ ID 82"
XX FN WO2004073657-A2.
XX PD 02-SEP-2004.
XX PF 19-FEB-2004; 2004WO-US005455.
XX PR 19-FEB-2003; 2003US-0448784P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX XZ Aziz N, Gish KC, Wilson KB, Zlotnik A;
XX FI WPI; 2004-652787/63.
XX DR P-PSDB; ADR46669.
XX PT Detecting a pathological cell in a patient for diagnosing or treating

cancer by detecting in a biological sample from the patient genes whose expression are up-regulated or down-regulated in specific cancers.

Claim 1; SEQ ID NO 24; 375pp; English.

The present invention relates to a method for detecting cancer in a patient. The method comprises detecting in a biological sample from the patient a nucleotide or protein sequence comprising a sequence that is at least 80% identical to a nucleotide sequence (AD46588-AD46645) or protein sequence (AD46646-AD46703). The method is useful for detecting cancer for preparing a composition for diagnosing or treating cancer.

Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;

Query Match	99.9%;	Score	1462.4;	DB	13;	Length	2010;
Best Local Similarity	99.9%;	Pred. No.	0;				
Matches	1463;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	1	ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACA	CTGTTTCCGAAAGACAAAT	60			
DB	282	ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACA	CTGTTTCCGAAAGACAAAT	341			
QY	61	ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGAGAT	TTGGATATCGAATCCAG	120			
DB	342	ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGAGAT	TTGGATATCGAATCCAG	401			
QY	121	ACCTGTGCTTCTGACTATCTTCTTCAACGAGCTTTCAGAT	CAATATGTCCTACTGT	180			
DB	402	ACCTGTGCTTCTGACTATCTTCTTCAACGAGCTTTCAGAT	CAATATGTCCTACTGT	461			
QY	181	GGAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGA	AGTAACCGTCCGCTTT	240			
DB	462	GGAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGA	AGTAACCGTCCGCTTT	521			
QY	241	GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGTA	CGTACCTATCGGAGCAGCAGAT	300			
DB	522	GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGTA	CGTACCTATCGGAGCAGCAGAT	581			
QY	301	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTT	TGGAAGACAGATAACACAAA	360			
DB	582	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTT	TGGAAGACAGATAACACAAA	641			
QY	361	TTCTGCCAGCTGTTGTAGACGCTAGCAGGAGACATTT	CTGGGAATATGGTAGGA	420			
DB	642	TTCTGCCAGCTGTTGTAGACGCTAGCAGGAGACATTT	CTGGGAATATGGTAGGA	701			
QY	421	TATAGATACCTCTTTATTTGCAAAAGCTGCCATCATGC	AGGAATATTTGCTGATGA	480			
DB	702	TATAGATACCTCTTTATTTGCAAAAGCTGCCATCATGC	AGGAATATTTGCTGATGA	761			
QY	481	CTAGGTGGCCAGATCAGTGTGCTTACGCGCAAGGGAT	CAGTCGATATGAAGGATTCG	540			
DB	762	CTAGGTGGCCAGATCAGTGTGCTTACGCGCAAGGGAT	CAGTCGATATGAAGGATTCG	821			
QY	541	GCCAAATGTTGTTTTCGAGGGATGTTCCCTGTGACACA	AGCGATTTCTGTTTACCTCC	600			
DB	822	GCCAAATGTTGTTTTCGAGGGATGTTCCCTGTGACACA	AGCGATTTCTGTTTACCTCC	881			
QY	601	AATGTTGACGACGATCTTGTAGTTTGAACCTGAGCGG	CAATCAGAGCTTCTTCCCTCA	660			
DB	882	AATGTTGACGACGATCTTGTAGTTTGAACCTGAGCGG	CAATCAGAGCTTCTTCCCTCA	941			
QY	661	TGCGCTGCGTCAATCAGAGTGGAGACCAAGTTTCACT	GGTCTCTGCGCAAGCCGACTT	720			
DB	942	TGCGCTGCGTCAATCAGAGTGGAGACCAAGTTTCACT	GGTCTCTGCGCAAGCCGACTT	1001			
QY	721	CAGGACCAAGGCCCATCATGCGGCTTCGGGCGACAGT	AGCAACCAACCAACAGAG	780			
DB	1002	CAGGACCAAGGCCCATCATGCGGCTTCGGGCGACAGT	AGCAACCAACCAACAGAG	1061			
QY	781	TGCGTGGAGATCGATTTGGGGGAGAAAGAAATTAAC	AGGAATTAAGGACCAAGATCT	840			
DB	1062	TGCGTGGAGATCGATTTGGGGGAGAAAGAAATTAAC	AGGAATTAAGGACCAAGATCT	1121			

QY	841	ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGT	GATGAACCTTCAAAAAACAATAAT	900
DB	1122	ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGT	GATGAACCTTCAAAAAACAATAAT	1181
QY	901	TCTAAGTGAAGACCTTATAAGGAATTTGCAATTAAT	GAAGAAAGGTGTTTCAGGGTAAC	960
DB	1182	TCTAAGTGAAGACCTTATAAGGAATTTGCAATTAAT	GAAGAAAGGTGTTTCAGGGTAAC	1241
QY	961	TCTAAGTTCGGGACCCAGTGCAGAAACAAATTTCA	TCTCCCAATCGTGGCCAGATATGTG	1020
DB	1242	TCTAAGTTCGGGACCCAGTGCAGAAACAAATTTCA	TCTCCCAATCGTGGCCAGATATGTG	1301
QY	1021	CGGGTGTCTCCCGACAGATGGCACCATGAGATAGCT	TGAAGTGGAGCTCATTTGGTTGC	1080
DB	1302	CGGGTGTCTCCCGACAGATGGCACCATGAGATAGCT	TGAAGTGGAGCTCATTTGGTTGC	1361
QY	1081	CAGATTACAAAGGTAATGATTCATTTGGTGGCGCA	AGACAAAGTCAAGCACCAAGTGT	1140
DB	1362	CAGATTACAAAGGTAATGATTCATTTGGTGGCGCA	AGACAAAGTCAAGCACCAAGTGT	1421
QY	1141	TCAACTTAAGAAAGAGATGAGACATCAAGGCCCAT	CCCCCTCGGAAGAAACATCCACA	1200
DB	1422	TCAACTTAAGAAAGAGATGAGACATCAAGGCCCAT	CCCCCTCGGAAGAAACATCCACA	1481
QY	1201	GGAAATAAACATTTACAAACGGTGGCTATTCCATT	GGTGGCTCTCTTGTGTTGGTTGGCT	1260
DB	1482	GGAAATAAACATTTACAAACGGTGGCTATTCCATT	GGTGGCTCTCTTGTGTTGGTTGGCT	1541
QY	1261	GGAAATGGGATCTTTGACGCTTTAGAAAGAAAGA	AGAAAGTCCGTATGGATCA	1320
DB	1542	GGAAATGGGATCTTTGACGCTTTAGAAAGAAAGA	AGAAAGTCCGTATGGATCA	1601
QY	1321	GGGAGGCTCAGAAAAACAGACTGTTGGAAGCAGAT	TAAATATCCCTTTGCCAGACATCAG	1380
DB	1602	GGGAGGCTCAGAAAAACAGACTGTTGGAAGCAGAT	TAAATATCCCTTTGCCAGACATCAG	1661
QY	1381	TCAGCTGAGCTTTTACCATCAGCTATGATAATGAG	AGGAGATGACACAAAAGTTAGATCTC	1440
DB	1662	TCAGCTGAGCTTTTACCATCAGCTATGATAATGAG	AGGAGATGACACAAAAGTTAGATCTC	1721
QY	1441	ATCACAAGTGTATGCGCAGGTTAA	1464	
DB	1722	ATCACAAGTGTATGCGCAGGTTAA	1745	

RESULT 8
ACD66718

ID ACD66718 standard; cdna; 2145 BP.

XX ACD66718;

XX AC ACD66718;

QY 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
|||
Db 1477 GCAGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1536
|||
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACAAAAGTTAGATCTC 1440
|||
Db 1537 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACAAAAGTTAGATCTC 1596
|||
QY 1441 ATCAAGTGTATGGCAGGTTA 1463
|||
Db 1597 ATCAAGTGTATGGCAGGTTA 1619
|||

RESULT 9

ADQ10135

ID ADQ10135 standard; CDNA; 2145 BP.

XX

AC ADQ10135;

XX

DT 09-SEP-2004 (first entry)

XX

DE Human polynucleotide #11.

XX

KW Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;
KW asthma; anaemia; graft-versus-host reaction; allergic reaction;
KW cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;
KW osteoarthritis; arteriosclerosis; hypertension; bacterial infection;
KW psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; AIDS; tuberculosis;
KW viral infection; malaria; goiter; infertility; endometriosis;
KW muscular disorder.

XX

OS Homo sapiens.

XX

PN US2004121396-A1.

XX

PD 24-JUN-2004.

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PF 19-DEC-2003; 2003US-00741790.

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PR 14-JUN-1999; 99US-00333159.

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PR 29-JUN-1999; 99US-00342364.

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PR 10-SEP-1999; 99US-00393996.

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PR 19-OCT-1999; 99US-00420707.

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PR 07-JAN-2000; 2000US-00479249.

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PR 27-APR-2000; 2000US-00559497.

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PR 24-MAY-2000; 2000US-00578063.

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PR 16-JUN-2000; 2000US-00596194.

XX

PR 23-JUN-2000; 2000US-00602871.

XX

PR 30-JUN-2000; 2000US-00608452.

XX

PR 12-JAN-2001; 2001US-00759130.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;

XX Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl AD;

XX WPI; 2004-479675/45.

XX

PT New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and

XX treating cancer, constipation, hemorrhoids, cystic fibrosis,

XX hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,

XX tuberculosis, malaria, goiter, infertility.

XX

PS Claim 2; SEQ ID NO 72; 483pp; English.

XX

CC The invention relates to human polynucleotides and the polypeptides they

XX encode. The invention also relates to a host cell containing a

XX polynucleotide of the invention, an antibody which selectively binds with

XX a polypeptide of the invention, a method of detecting the presence of a

XX polypeptide in a sample, a method of identifying a compound which binds

XX with a polypeptide, and a method of modulating the activity of a

CC polypeptide. The polynucleotides, polypeptides and compositions are
CC useful for diagnosing, preventing and/or treating cancer, obesity,
CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,
CC infertility, endometriosis, wounds and muscular disorders. This sequence
CC represents a human polynucleotide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 2145 BP; 556 A; 561 C; 575 G; 453 T; 0 U; 0 Other;

Query Match 99.7%; Score 1459.8; DB 12; Length 2145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTGCGAAGACAAATT 60
|||
Db 157 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTGCGAAGACAAATT 216
|||

QY 61 ACAGTACCAAGGGGAAAGACTGATTCTGAGTTGGGAGATTGGATATCGAATCCAG 120
|||
Db 217 ACAGTACCAAGGGGAAAGACTGATTCTGAGTTGGGAGATTGGATATCGAATCCAG 276
|||

QY 121 ACCTGTCTTCTGACTATCTTCTTCCACAGCTTCTCAGATCAATATGTTCCATCTGT 180
|||
Db 277 ACCTGTCTTCTGACTATCTTCTTCCACAGCTTCTCAGATCAATATGTTCCATCTGT 336
|||

QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAGTGAAGTAACCGTCCGCTTT 240
|||
Db 337 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACAGTGAAGTAACCGTCCGCTTT 396
|||

QY 241 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTCTGACCTATCGGAGCAGCACCAT 300
|||
Db 397 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTCTGACCTATCGGAGCAGCACCAT 456
|||

QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTGAAAGACAGAAATCAGCAAA 360
|||
Db 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTGAAAGACAGAAATCAGCAAA 516
|||

QY 361 TTCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGGTAGATGA 420
|||
Db 517 TTCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGGTAGATGA 576
|||

QY 421 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAAGAAATAATTGCTGATGA 480
|||
Db 577 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAAGAAATAATTGCTGATGA 636
|||

QY 481 CTAGTGGCCAGATCAGTGTCTTCCGCAAGGGATCAGTCGATATGAAGGATCTTG 540
|||
Db 637 CTAGTGGCCAGATCAGTGTCTTCCGCAAGGGATCAGTCGATATGAAGGATCTTG 696
|||

QY 541 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACTCC 600
|||
Db 697 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACTCC 756
|||

QY 601 AATGGTTGCAGAGATCCCTTGGAGTTTGAACCTGACGGGCAATACAGAGCTTCTTCTCA 660
|||
Db 757 AATGGTTGCAGAGATCCCTTGGAGTTTGAACCTGACGGGCAATACAGAGCTTCTTCTCA 816
|||

QY 661 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCTGCTCTGCGCCAGGCCACTTT 720
|||
Db 817 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCTGCTCTGCGCCAGGCCACTTT 876
|||

QY 721 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGTAGCAACAACCAAAACCCAGAGAG 780
|||
Db 877 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGTAGCAACAACCAAAACCCAGAGAG 936
|||

QY 781 TGGCTGGAGATCGATTTTGGGGGAGAAAAAAGAAATTAACAGGAATTAGGACCACAGGATCT 840
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[illegible]

RESULT 10

RESULI I
ADI28055

AD128055
ID AD128055 standard: cDNA: 2888 bp.

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CC007104

AC ADI28055:

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84

DT 15-APR-2004 (first entry)

XX

ECMAD gene clone 184661CB1.

systemic lupus erythematosus; ulcerative colitis; uveitis; neurological disorder; epilepsy; stroke; Alzheimer's disease; Huntington's disease; Parkinson's disease; multiple sclerosis; meningitis; periodic paralysis; mental disorder; mood; anxiety; schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder; osteoporosis; Paget's disease; osteonecrosis; osteomyelitis; chondrosarcoma; giant cell tumor; psoriatic arthritis; infectious arthritis; systemic sclerosis; cell proliferative disorder; actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.

Homo sapiens.

• അനുകൂലമായ ചിന്ത

WO200202634-

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10-JAN-2002.

29-JUN-2001; 2001WO-US021067.

30-JUN-2000; 2000US-0215454P.

18-JUL-2000; 2000US-0219462P.

12-OCT-2000; 2000US-0240106P.

12-OCT-2000; 2000US-0240111F

27-OCT-2000; 2000US-0244021P

14-NOV-2000; 2000US-
15-NOV-2000; 2000US-

16-NOV-2000; 2000

(INCY-) INCYTE GENOMICS INC.

Tang YT, Yue H, Azimzai Y, He A, Batra S, Lo TP, Nguyen DB;
Burtrill JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kearney L;
Burford N, Yao MG, Wallia NK, Elliot VS, Patterson C, Khan FA;
Baughn MR, Hafalia AJA, Policky JL, Au-Young J, Lu Y, Borowsky ML;
Lu DAM, Ramkumar J, Yang J, Gururajan R, Warren BA, Gietzen K;
Xu Y, Kallick DA, Lee EA, Thangaveilu K, Delegeane AM, Lee S;
WPI: 2002-154732/20.

Novel isolated human extracellular matrix and cell adhesion molecules useful for treating, preventing connective tissue disorder e.g. osteoporosis, Paget's disease, genetic disorder e.g. cystic fibrosis, thalassaemia.

Claim 11: SEO ID NO 47: 270pp: English:

SQ		Sequence 2888 BP; 736 A; 696 C; 775 G; 681 T; 0 U; 0 Other;	
Query Match		99.7%; Score 1459.8; DB 6; Length 2888;	
Best Local Similarity		99.9%; Pred. No. 0;	
Matches 1461; Conservative		0; Mismatches 2; Indels 0; Gaps 0;	
QY	1	ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTGCAGAAAGACAAATT	60
DB	282	ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTGCAGAAAGACAAATT	341
QY	61	ACAGTACCAAGGGGAAAAGACATGATCTCGAGGTGGGAGATTGGATATCGAATCCAG	120
DB	342	ACAGTACCAAGGGGAAAAGACATGATCTCGAGGTGGGAGATTGGATATCGAATCCAG	401
QY	121	ACCTGTGCTTCTGACTATCTTCTTCCACCAGCTCTTCAGATCAATATGTCATATCTGT	180
DB	402	ACCTGTGCTTCTGACTATCTTCTTCCACCAGCTCTTCAGATCAATATGTCATATCTGT	461
QY	181	GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT	240
DB	462	GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT	521
QY	241	GAGAGTGGATCCCAATCTTCTGCGGGGTTTTTGTGCTGACCTATGGGAGCAGGACCAT	300
DB	522	GAGAGTGGATCCCAATCTTCTGCGGGGTTTTTGTGCTGACCTATGGGAGCAGGACCAT	581
QY	301	CCAGATTATTAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA	360
DB	582	CCAGATTATTAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA	641
QY	361	TTCTGCCAGCTGTTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA	420
DB	642	TTCTGCCAGCTGTTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA	701
QY	421	TATAGATACCTCTTTATTTGCGAAAGCTGCCATCCATCGACGAATAATTGCTGATGAA	480
DB	702	TATAGATACCTCTTTATTTGCGAAAGCTGCCATCCATCGACGAATAATTGCTGATGAA	761
QY	481	CTAGGTGGCCAGATCAGTGTCTTACGCGCAAGAGGATCAGTCGATATGAAGGATTCG	540
DB	762	CTAGGTGGCCAGATCAGTGTCTTACGCGCAAGAGGATCAGTCGATATGAAGGATTCG	821
QY	541	GCCAAATGGTGTCTTTTCGAGGATGTTTCCCTGTCCAGACAAGCGATTTCTGTTTACCTCC	600
DB	822	GCCAAATGGTGTCTTTTCGAGGATGTTTCCCTGTCCAGACAAGCGATTTCTGTTTACCTCC	881
QY	601	AATGGTTGACGAGATCTTGAATTTTGAACCTGACGGGCAATCAGAGCTTCTCCCTCA	660
DB	882	AATGGTTGACGAGATCTTGAATTTTGAACCTGACGGGCAATCAGAGCTTCTCCCTCA	941
QY	661	TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTTCACTGTTCTCTGGCCAAAGCCGACTT	720
DB	942	TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTTCACTGTTCTCTGGCCAAAGCCGACTT	1001
QY	721	CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACAACCAACCAACCGAGAG	780
DB	1002	CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACAACCAACCAACCGAGAG	1061
QY	781	TGGCTCGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAAGGACCAAGATCT	840
DB	1062	TGGCTCGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAAGGACCAAGATCT	1121
QY	841	ACACAGTCCGAATCTCAACTTTTATGTTTGAAGTGTGATGAATTCATTAACCAATAT	900
DB	1122	ACACAGTCCGAATCTCAACTTTTATGTTTGAAGTGTGATGAATTCATTAACCAATAT	1181
QY	901	TCTAAGTGGAAAGCTTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAC	960
DB	1182	TCTAAGTGGAAAGCTTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAC	1241
QY	961	TCTAAGTGGAAAGCTTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAC	1020
DB	1242	TCTAAGTGGAAAGCTTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAC	1301

QY	1021	CGGGTTGTCCCCAGACATGGCACCAGAGATAGCCCTTGAAGCTGGAGCTCATTTGGTTGC	1080
DB	1302	CGGGTTGTCCCCAGACATGGCACCAGAGATAGCCCTTGAAGCTGGAGCTCATTTGGTTGC	1361
QY	1081	CAGATTACACAAGGTAATGATTTCATTTGGTGGCGCAAGCAAAAGTCAAAAGCACCAGTGT	1140
DB	1362	CAGATTACACAAGGTAATGATTTCATTTGGTGGCGCAAGCAAAAGTCAAAAGCACCAGTGT	1421
QY	1141	TCNACTAAGAAAGAAAGATGAGACAATCAGACAGGCCCATCCCTCGGAAGAAAACATCCACA	1200
DB	1422	TCNACTAAGAAAGAAAGATGAGACAATCAGACAGGCCCATCCCTCGGAAGAAAACATCCACA	1481
QY	1201	GGAAATAAAACATTACAAACGGTGGCTATTCCATTGGTGTCTCTTGTCTCTGGTGTGTGCT	1260
DB	1482	GGAAATAAAACATTACAAACGGTGGCTATTCCATTGGTGTCTCTTGTCTCTGGTGTGTGCT	1541
QY	1261	GGAAATGGGATCTTTTCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA	1320
DB	1542	GGAAATGGGATCTTTTCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA	1601
QY	1321	GGGAGGCTCAGAAAACAGACTGTTGGAAAGCAGATTAAATATCCCTTTGCCACACATCAG	1380
DB	1602	GGGAGGCTCAGAAAACAGACTGTTGGAAAGCAGATTAAATATCCCTTTGCCACACATCAG	1661
QY	1381	TCAGCTGAGTTTACCATCAGCTATGATAATGAAAGGAGATGACACAAAGTTAGATCTC	1440
DB	1662	TCAGCTGAGTTTACCATCAGCTATGATAATGAAAGGAGATGACACAAAGTTAGATCTC	1721
QY	1441	ATCACAAGTGTATGGCAGGTTA	1463
DB	1722	ATCACAAGTGTATGGCAGATT	1744
RESULT 11			
ID	ABN86493		
XX	ABN86493 standard; cDNA; 3151 BP.		
AC	ABN86493;		
XX			
DT	21-OCT-2002 (first entry)		
XX			
DE	Human neurophilin homologue polypeptide, zcub5 encoding cDNA.		
XX			
KW	Neurophilin; zcub5; human; antitumor; antidiabetic; ophthalmological;		
KW	antiatherosclerotic; antipsoriatic; antirheumatic; antithrombotic; gene;		
KW	cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;		
XX	cytostatic; gene therapy; ss.		
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
CDS	76..2223	/*tag= a	
FT		/product= "zcub5"	
XX			
PN	WO200253739-A2.		
XX			
PD	11-JUL-2002.		
XX			
PF	15-NOV-2001; 2001WO-US045542.		
XX			
PR	15-NOV-2000; 2000US-0249004P.		
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Fox BA, Gao Z, Shoemaker KE;		
XX			
DR	WPI; 2002-590634/63.		
DR	P-PSDB; ABB81000.		
XX			
PT	Novel isolated neurophilin homolog polypeptide, termed zcub5, useful in		
PT	diagnosis or treatment of disorders associated with abnormal cell		

601 AATGGTTGCAGCAGATCCTTGGAGTTTGAACCTGACGGGCAAATCAGAGCTTCTTCCCTCA 660

Human; TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung;
KW
skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
KW
bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
KW

[illegible]

Human; TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung;
KW
skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
KW
bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
KW

anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; ss;
malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
muscular dystrophy; immuno-competence; vertebrae; blood; serum.

Homo sapiens.

Key Location/Qualifiers

CDS 72..2219

/*tag= a

/product= "Human TANGO 229"

72..173

/*tag= b

174..2216

/*tag= c

/product= "Mature human TANGO 229"

W0200129088-AL.

XX

XX

PD 26-APR-2001.

XX

XX 23-JUN-2000; 2000WO-US017386.

XX

XX 19-OCT-1999; 99US-00420707.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby KR;

XX

XX WPI; 2001-308477/32.

XX

XX P-PSDB; AAU00670.

XX

XX New isolated nucleic acid molecule for diagnosis, prevention, and therapy

XX

XX of human and other animal disorder, or as modulating agent for regulating

XX

XX cellular processes.

XX

XX Claim 1; Fig 1; 263pp; English.

XX

XX The sequence represents a cDNA which encodes human TANGO 229 polypeptide.

XX

XX This protein and similar others exhibit the ability to affect growth,

XX

XX proliferation, survival, differentiation, activity, morphology, or

XX

XX movement/migration of, e.g. T cells and cells of the heart, liver,

XX

XX pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph

XX

XX node, peripheral blood leukocyte, bone marrow or thymus tissue. They can

XX

XX be used as modulating agents for regulating cellular processes, thus, the

XX

XX proteins and their associated nucleic acids can be used to prognosticate,

XX

XX prevent, diagnose, or treat disorders associated with physiological

XX

XX processes. These disorders include abnormal blood coagulation, asthma,

XX

XX anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery

XX

XX disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis,

XX

XX meningitis, attention deficit disorder, Crohn's disease, gastroenteritis,

XX

XX goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary

XX

XX embolism and muscular dystrophy. Antibodies to disorders such as these

XX can be made by providing a polypeptide of the invention to an immuno-

XX competent vertebrate and harvesting blood or serum from the vertebrate

XX

XX Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

XX

XX Query Match 99.7%; Score 1459.8; DB 4; Length 3594;

XX Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

QY 1 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCCGGAAGACAAATT 60

DB 228 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCCGGAAGACAAATT 287

QY 61 ACAGTACCAAGGGGAAAGACGATTCTGAGGTGGGAGATTGGATATCGAATCCCAG 120

DB 288 ACAGTACCAAGGGGAAAGACGATTCTGAGGTGGGAGATTGGATATCGAATCCCAG 347

QY 121 ACCTGTGCTTCGACTATCTCTTCCACGAGCTCTTCAGATCAATATGGTCCATACTGT 180

DB

DB 348 ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTTCAGATCAATATGGTCCATACTGT 407

QY 181 GGAAGTATGACTCTTCCCAAGAACCTCTGTTTGAACAACAAGTGAAGTAAACCGTCCGCTTT 240

DB 408 GGAAGTATGACTCTTCCCAAGAACCTCTGTTTGAACAACAAGTGAAGTAAACCGTCCGCTTT 467

QY 241 GAGAGTGGATCCCAACATTTCTGGCCGGGGTTTTTGTGTCACCTATGCGAGCAGCGACCAT 300

DB 468 GAGAGTGGATCCCAACATTTCTGGCCGGGGTTTTTGTGTCACCTATGCGAGCAGCGACCAT 527

QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTGGAAGACAGAAATACAGCAA 360

DB 528 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTGGAAGACAGAAATACAGCAA 587

QY 361 TTCTGCCCGAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420

DB 588 TTCTGCCCGAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 647

QY 421 TATAGAGATACCTCTTTTATTGTGCAAAAGCTGCCATCCATGCAGGAATAATTTGCTGATGAA 480

DB 648 TATAGAGATACCTCTTTTATTGTGCAAAAGCTGCCATCCATGCAGGAATAATTTGCTGATGAA 707

QY 481 CTAGGTGGCCAGATCAGTGTCTTCCAGCGCAAAAGGATCAGTCGATATGAAGGATTTCTG 540

DB 708 CTAGGTGGCCAGATCAGTGTCTTCCAGCGCAAAAGGATCAGTCGATATGAAGGATTTCTG 767

QY 541 GCCAATGGTGTCTTCTTCCGAGGATGTTCCCTGTGAGACAAAGGATTTCTGTTTACCTCC 600

DB 768 GCCAATGGTGTCTTCTTCCGAGGATGTTCCCTGTGAGACAAAGGATTTCTGTTTACCTCC 827

QY 601 AATGGTTGCAGCAGATCCTTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCTCA 660

DB 828 AATGGTTGCAGCAGATCCTTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCTCA 887

QY 661 TGCCAGTGGTCAATCAGAGTGGAGACCAAGTTTCACTGTGTCCTTGGCCAAAGCCGACTT 720

DB 888 TGCCAGTGGTCAATCAGAGTGGAGACCAAGTTTCACTGTGTCCTTGGCCAAAGCCGACTT 947

QY 721 CAGGACCAAGGCCCATCATGGGCTTCGGGGCAGTAGCAACCAACCAACCAACCAACGAG 780

DB 948 CAGGACCAAGGCCCATCATGGGCTTCGGGGCAGTAGTAGCAACCAACCAACCAACGAG 1007

QY 781 TGCTCGAGATCGATTTGGGGGAGAAAAAATAACAGGAATATTAGGACCAACGAGATCT 840

DB 1008 TGCTCGAGATCGATTTGGGGGAGAAAAAATAACAGGAATATTAGGACCAACGAGATCT 1067

QY 841 ACACAGTGGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 900

DB 1068 ACACAGTGGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 1127

QY 901 TCTAAGTGGAAAGACCTATTAAGGAATTTGTAATTAAGGAAGGTTTTCAGGGTTAC 960

DB 1128 TCTAAGTGGAAAGACCTATTAAGGAATTTGTAATTAAGGAAGGTTTTCAGGGTTAC 1187

QY 961 TCTAAGTGGAAAGACCTATTAAGGAATTTGTAATTAAGGAAGGTTTTCAGGGTTAC 1020

DB 1188 TCTAAGTGGAAAGACCTATTAAGGAATTTGTAATTAAGGAAGGTTTTCAGGGTTAC 1247

QY 1021 CGGGTTGTCCCGCAGACATGGCACCAAGAGATAGCTTTGAAGTGGAGCTCATTTGGTTGC 1080

DB 1248 CGGGTTGTCCCGCAGACATGGCACCAAGAGATAGCTTTGAAGTGGAGCTCATTTGGTTGC 1307

QY 1081 CAGATTTACACAGGTTAATGATTTCAATTTGGTGTGGCGCAAGCAAGTCAAGCAACAGTGT 1140

DB 1308 CAGATTTACACAGGTTAATGATTTCAATTTGGTGTGGCGCAAGCAAGTCAAGCAACAGTGT 1367

QY 1141 TCAACTTAAGAAAGAGATGAGCAATCAAGAGCCCATCCCTCGGAAGAAACATCCACA 1200

DB 1368 TCAACTTAAGAAAGAGATGAGCAATCAAGAGCCCATCCCTCGGAAGAAACATCCACA 1427

QY 1201 GGAATAAAACATTACACCGTGGCTATTCCATTTGGTGTCTCTTGTGTTGCTGGTGTGCT 1260

DB 1428 GGAATAAAACATTACACCGTGGCTATTCCATTTGGTGTCTCTTGTGTTGCTGGTGTGCT 1487

Qy 1261 GGAATGGGATCTTTGACGCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
Db |||||
Qy 1488 GGAATGGGATCTTTGACGCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGATCA 1547
Db |||||
Qy 1321 GCGAGGCTCAGAAAACAGACTGTTGAAGCAGATTAAATATCCCTTGGCAGATCAG 1380
Db |||||
Qy 1548 GCGAGGCTCAGAAAACAGACTGTTGAAGCAGATTAAATATCCCTTGGCAGATCAG 1607
Db |||||
Qy 1381 TCAGTCAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db |||||
Qy 1608 TCAGTCAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1667
Db |||||
Qy 1441 ATCACAAGTATGATGCGAGTTA 1463
Db |||||
Qy 1668 ATCACAAGTATGATGCGAGTTA 1690
Db |||||

RESULT 13

ACD66717

ID ACD66717 standard; cDNA; 3594 BP.

XX AC ACD66717;

XX AC ACD66717;

XX 17-SEP-2003 (first entry)

XX DT

XX DE

XX Secreted polypeptide-related cDNA #9.

XX Human; gene; ss: TANGO; INTERCEPT; secreted polypeptide; immune disorder;
XX hormonal disorder; proliferative disorder; cancer; thyroid disorder;
XX diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
XX myocardial infarction; congestive heart disease; blood platelet disorder;
XX thrombocytopenia; blood vessel; atherosclerosis; vasculitis.

XX Homo sapiens.
XX OS

XX US2003022279-A1.
XX PN

XX 30-JAN-2003.
XX PD

XX 12-JAN-2001; 2001US-00759130.
XX PF

XX 14-JUN-1999; 99US-00333159.
XX PR

XX 29-JUN-1999; 99US-00342364.
XX PR

XX 10-SEP-1999; 99US-00393996.
XX PR

XX 19-OCT-1999; 99US-00420707.
XX PR

XX 07-JAN-2000; 2000US-00479249.
XX PR

XX 27-APR-2000; 2000US-00559497.
XX PR

XX 24-MAY-2000; 2000US-00578063.
XX PR

XX 16-JUN-2000; 2000US-00596194.
XX PR

XX 23-JUN-2000; 2000US-00602871.
XX PR

XX 30-JUN-2000; 2000US-00608452.
XX PR

XX (FRAS/) FRASER C C.
XX PA

XX (BARN/) BARNES T M.
XX PA

XX (SHAR/) SHARP J D.
XX PA

XX (KIRS/) KIRST S J.
XX PA

XX (MYER/) MYERS P S.
XX PA

XX (LEIB/) LEIBY K R.
XX PA

XX (HOLT/) HOLTZMAN D A.
XX PA

XX (MCC/) MCCARTHY S A.
XX PA

XX (WRIG/) WRIGHTON N.
XX PA

XX (MACK/) MACKAY C R.
XX PA

XX (GOOD/) GOODEARL A D J.
XX PA

XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
XX Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
XX WPI; 2003-456290/43.
XX DR P-PSDB; ABO32527.
XX XX

XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
XX PI

PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
PT forensic biology.

XX Claim 2; Fig 10A-10F; 482pp; English.

XX The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related cDNA of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Query Match 99.7%; Score 1459.8; DB 8; Length 3594;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 60

Db |||||

Qy 228 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 287

Db |||||

Qy 61 ACAGTACCAGGAGGAGAAAGACTGATTCTGAGGTTGGAGATTGGATATCGAATCCAG 120

Db |||||

Qy 288 ACAGTACCAGGAGGAGAAAGACTGATTCTGAGGTTGGAGATTGGATATCGAATCCAG 347

Db |||||

Qy 121 ACCTGTGCTTCTGACTATCTTCTCTTCCACAGCTCTTCCAGATCAATATGGTCCATCTGT 180

Db |||||

Qy 348 ACCTGTGCTTCTGACTATCTTCTCTTCCACAGCTCTTCCAGATCAATATGGTCCATCTGT 407

Db |||||

Qy 181 GGAAGTATGACTGTTTCCAAAAGAACTCTTGTGAAACAAAGTGAAGTAAACCGTCCGTTT 240

Db |||||

Qy 408 GGAAGTATGACTGTTTCCAAAAGAACTCTTGTGAAACAAAGTGAAGTAAACCGTCCGTTT 467

Db |||||

Qy 241 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 300

Db |||||

Qy 468 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 527

Db |||||

Qy 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGAAA 360

Db |||||

Qy 528 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGAAA 587

Db |||||

Qy 361 TTCTGCCCCAGCTGGTTGTAGAGAGCTAGAGAGAGACATTTCTGGGAATATGGTAGATGA 420

Db |||||

Qy 588 TTCTGCCCCAGCTGGTTGTAGAGAGCTAGAGAGAGACATTTCTGGGAATATGGTAGATGA 647

Db |||||

Qy 421 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCAGGAATAATTTGCTGATGAA 480

Db |||||

Qy 648 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCAGGAATAATTTGCTGATGAA 707

Db |||||

Qy 481 CTAGGTGGCCAGATCAGTGTCTTTCAGCCAAAGGGATCAGTCGATGATGAAGGAATCTG 540

Db |||||

Qy 708 CTAGGTGGCCAGATCAGTGTCTTTCAGCCAAAGGGATCAGTCGATGATGAAGGAATCTG 767

Db |||||

Qy 541 GCCAATGGTGTCTTTTCAGGGATGGTTCCCTGTCCAGACAGCGATTTCTGTTTACCTCC 600

Db |||||

Qy 768 GCCAATGGTGTCTTTTCAGGGATGGTTCCCTGTCCAGACAGCGATTTCTGTTTACCTCC 827

Db |||||

Qy 601 AATGGTTGACGACGATCCTTTGAGTTTGTGAACCTGACCGGAAATCAGAGCTTCTTCTCTCA 660

Db |||||

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Db 828 AATGGTTGCAGCAGATCCTTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCTCA 887
Qy 661 TGGCAGTCGTCATGAGAGTGGAGACCAAGTTCACCTGCTCTCTGCGCAAGCCGACCTT 720
Db 888 TGGCAGTCGTCATGAGAGTGGAGACCAAGTTCACCTGCTCTCTGCGCAAGCCGACCTT 947
Qy 721 CAGGACCAAGCCCATCATGGCTTCGGGGGAGCAAGTAGCAACCAACCAACCAACCAAGAG 780
Db 948 CAGGACCAAGCCCATCATGGCTTCGGGGGAGCAAGTAGCAACCAACCAACCAACCAAGAG 1007
Qy 781 TGGCTGAGATCGATTTGGGGGAGCAAGTAGCAACCAACCAACCAACCAAGATCT 840
Db 1008 TGGCTGAGATCGATTTGGGGGAGCAAGTAGCAACCAACCAACCAACCAAGATCT 1067
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTTGAAGTTCCTGATGAACTTCAAAAACAATAAT 900
Db 1068 ACACAGTCGAACCTTCAACTTTTATGTTTGAAGTTCCTGATGAACTTCAAAAACAATAAT 1127
Qy 901 TCTAAGTGGAGACCTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAAC 960
Db 1128 TCTAAGTGGAGACCTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAAC 1187
Qy 961 TCTAAGTGGAGACCTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAAC 1020
Db 1188 TCTAAGTGGAGACCTATAAGGAATTTGAATAATGAAGAAAGTGTTCAGGGTAAAC 1247
Qy 1021 CGGGTTGTCCCGCAGACATGCGCAGGATGACCTTGAAGTGGAGCTCATTTGGTTGC 1080
Db 1248 CGGGTTGTCCCGCAGACATGCGCAGGATGACCTTGAAGTGGAGCTCATTTGGTTGC 1307
Qy 1081 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAGCAGGATTT 1140
Db 1308 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAGCAGGATTT 1367
Qy 1141 TCAACTAAGAAAGAGATGAGACATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1368 TCAACTAAGAAAGAGATGAGACATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1427
Qy 1201 GGAATAAACATTACAGGTTGCTATTCCATTCGTCCTCTCTGTCCTGCTGTTGCT 1260
Db 1428 GGAATAAACATTACAGGTTGCTATTCCATTCGTCCTCTCTGTCCTGCTGTTGCT 1487
Qy 1261 GGAATGGGATCTTTGAGAGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1488 GGAATGGGATCTTTGAGAGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1547
Qy 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTGCCAGACATCAG 1380
Db 1548 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTGCCAGACATCAG 1607
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAGTTAGATCTC 1440
Db 1608 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAGTTAGATCTC 1667
Qy 1441 ATCAAGTGTATGGCAGGTTA 1463
Db 1668 ATCAAGTGTATGGCAGGTTA 1690
```

RESULT 14

ADQ10134

ID ADQ10134 standard; cdna; 3594 BP.

XX AC

XX ADQ10134;

XX AC

DT 09-SEP-2004 (first entry)

DE Human polynucleotide #10.

XX AC

Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;
asthma; anaemia; graft-versus-host reaction; allergic reaction;
cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;
osteoarthritis; arteriosclerosis; hypertension; bacterial infection;

KW

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SQ

Query Match

Best Local Similarity

Matches 1461;

Conservative

0; Mismatches

2; Indels

0; Gaps

0; Other;

99.7%; Score 1459.8;

DB 12; Length 3594;

99.9%; Pred. No. 0;

0; Mismatches

2; Indels

0; Gaps

0; Other;

psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;
Huntington's disease; Parkinson's disease; AIDS; tuberculosis;
viral infection; malaria; goiter; infertility; endometriosis;
muscular disorder.

Homo sapiens.

US2004121396-A1.

24-JUN-2004.

19-DEC-2003; 2003US-00741790.

14-JUN-1999; 99US-00333159.

29-JUN-1999; 99US-00342364.

10-SEP-1999; 99US-00393996.

PR 07-OCT-1999; 99US-00420707.

PR 17-JAN-2000; 2000US-00479249.

PR 27-APR-2000; 2000US-00559497.

PR 24-MAY-2000; 2000US-00578063.

PR 15-JUN-2000; 2000US-00596194.

PR 23-JUN-2000; 2000US-00602871.

PR 30-JUN-2000; 2000US-00608452.

PR 12-JAN-2001; 2001US-00759130.

(MILL-) MILLENNIUM PHARM INC.

Fraser CC, Barnes TM, Sharp JD, KIRST SJ, Myers PS, Leiby KR;

Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;

WPI; 2004-479675/45.

New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and

treating cancer, constipation, hemorrhoids, cystic fibrosis,

hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,

tuberculosis, malaria, goiter, infertility.

Claim 2; SEQ ID NO 71; 483pp; English.

The invention relates to human polynucleotides and the polypeptides they

encode. The invention also relates to a host cell containing a

polynucleotide of the invention, an antibody which selectively binds with

a polypeptide of the invention, a method of detecting the presence of a

polypeptide in a sample, a method of identifying a compound which binds

with a polypeptide, and a method of modulating the activity of a

polypeptide. The polynucleotides, polypeptides and compositions are

useful for diagnosing, preventing and/or treating cancer, obesity,

gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host

reactions, allergic reactions, cystic fibrosis, hypogonadism,

cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,

hypertension, bacterial infections, psoriasis, diabetes mellitus,

hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's

disease, AIDS, tuberculosis, viral infections, malaria, goiter,

infertility, endometriosis, wounds and muscular disorders. This sequence

represents a human polynucleotide of the invention. Note: The sequence

data for this patent did not form part of the printed specification but

was obtained in electronic format from USPTO at

seqdata.uspto.gov/sequence.html.

Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Query Match

Best Local Similarity

Matches 1461;

Conservative

0; Mismatches

2; Indels

0; Gaps

0; Other;

99.7%; Score 1459.8;

DB 12; Length 3594;

99.9%; Pred. No. 0;

0; Mismatches

2; Indels

0; Gaps

0; Other;

1 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTTCGGAAGACAATT 60

228 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTTCGGAAGACAATT 287

61 ACAGTACCAAGGGGAAAGACATGATTCGAGTTGGGAGATTGGATATCGAATCCAG 120

288 ACAGTACCAAGGGGAAAGACATGATTCGAGTTGGGAGATTGGATATCGAATCCAG 347

marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences.

Sequence 3676 BP; 967 A; 841 C; 953 G; 914 T; 0 U; 1 Other;

Query Match	99.7%;	Score 1459.8;	DB 5;	Length 3676;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1461; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	ATGACATCTAGAAATTATCCCGGAGACCTTACCCCAATCACACTGTTTGGCGAAAGACAATT	60	
DB	294	ATGACATCTAGAAATTATCCCGGAGACCTTACCCCAATCACACTGTTTGGCGAAAGACAATT	353	
QY	61	ACAGTACCAAGGGGAAAGAGACTGATTTCTGAGGTTTGGGAGATTTTGGATATCGAATCCCGAC	120	
DB	354	ACAGTACCAAGGGGAAAGAGACTGATTTCTGAGTGTGGGAGATTTGGATATCGAATCCCGAC	413	
QY	121	ACCTGTGCTTCTGACTATCTTCTCTTCAACAGCTCTTCAGATCAATATGGTCCACTACTGT	180	
DB	414	ACCTGTGCTTCTGACTATCTTCTCTTCAACAGCTCTTCAGATCAATATGGTCCACTACTGT	473	
QY	181	GGAAAGTATGACTGTTTCCCAAGAACTCTGTTTGAACACAAGTGAAGTAAACCGTCGCGCTTT	240	
DB	474	GGAAAGTATGACTGTTTCCCAAGAACTCTGTTTGAACACAAGTGAAGTAAACCGTCGCGCTTT	533	
QY	241	GAGAGTGGATCCCAATTTCTTGGCGCGGGGTTTTTGTCTGACCTATGCGAGCAGCGACCAT	300	
DB	534	GAGAGTGGATCCCAATTTCTTGGCGCGGGGTTTTTGTCTGACCTATGCGAGCAGCGACCAT	593	
QY	301	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTAATTGAAGACAGAAATACAGCAAA	360	
DB	594	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTAATTGAAGACAGAAATACAGCAAA	653	
QY	361	TTCTGCCCCAGCTGGTCTGAGAGAGTACGACGAGAGACATTTCTGGGAATATGGTAGATGGA	420	
DB	654	TTCTGCCCCAGCTGGTCTGAGAGAGTACGACGAGAGACATTTCTGGGAATATGGTAGATGGA	713	
QY	421	TATAGAGATACCTCTTTATTGTGCAAAAGCTCCCATCCATGACGAGGAATTAATTGCTGATGAA	480	
DB	714	TATAGAGATACCTCTTTATTGTGCAAAAGCTCCCATCCATGACGAGGAATTAATTGCTGATGAA	773	
QY	481	CTAGTGGCCAGATCAGTGTGCTTTACGCGCAAGAGGATCATGATATGAAGGGGATCTTG	540	
DB	774	CTAGTGGCCAGATCAGTGTGCTTTACGCGCAAGAGGATCATGATATGAAGGGGATCTTG	833	
QY	541	GCCAAATGGTGTCTTTTCGAGGGATGGTTTCCCTGTGACAGACAGCGATTTCTGTTTACCTCC	600	
DB	834	GCCAAATGGTGTCTTTTCGAGGGATGGTTTCCCTGTGACAGACAGCGATTTCTGTTTACCTCC	893	
QY	601	AATGGTTGACGACGATCCTTGAGTTTTGAAACCTGACGCGGCAAAATCAGAGCTTTCTTCTCA	660	
DB	894	AATGGTTGACGACGATCCTTGAGTTTTGAAACCTGACGCGGCAAAATCAGAGCTTTCTTCTCA	953	
QY	661	TGGCAGTTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGGCCAAAGCCCGACTT	720	
DB	954	TGGCAGTTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGGCCAAAGCCCGACTT	1013	

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